

673 671 669 667 665 663 661 659 657 655 653 651 649 647 645 643 641 639 637 635 633 631 629 627 625 623 621 619 617 615 613 611 609 607 605 603 601 599 597 595 593 591 589 587 585 583 581 579 577 575 573 571 569 567 565 563 561 559 557 555 553 551 549 547 545 543 541 539 537 535 533 531 529 527 525 523 521 519 517 515 513 511 509 507 505 503 501 499 497 495 493 491 489 487 485 483 481 479 477 475 473 471 469 467 465 463 461 459 457 455 453 451 449 447 445 443 441 439 437 435 433 431 429 427 425 423 421 419 417 415 413 411 409 407 405 403 401 399 397 395 393 391 389 387 385 383 381 379 377 375 373 371 369 367 365 363 361 359 357 355 353 351 349 347 345 343 341 339 337 335 333 331 329 327 325 323 321 319 317 315 313 311 309 307 305 303 301 299 297 295 293 291 289 287 285 283 281 279 277 275 273 271 269 267 265 263 261 259 257 255 253 251 249 247 245 243 241 239 237 235 233 231 229 227 225 223 221 219 217 215 213 211 209 207 205 203 201 199 197 195 193 191 189 187 185 183 181 179 177 175 173 171 169 167 165 163 161 159 157 155 153 151 149 147 145 143 141 139 137 135 133 131 129 127 125 123 121 119 117 115 113 111 109 107 105 103 101 99 97 95 93 91 89 87 85 83 81 79 77 75 73 71 69 67 65 63 61 59 57 55 53 51 49 47 45 43 41 39 37 35 33 31 29 27 25 23 21 19 17 15 13 11 9 7 5 3 1

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
R40-3-40B2-IR	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--
R40-4-40B12-IR	IRDMHYVWQDRDRYINGVRQWYISDRYNPGSAFYRWFID	40.3	9.0	2.0	0.2
R40-4-40G11-IR	RMGLQALAHYRKSAGPIFLSSGSVIKGSEGDPPFYAWFRLQ	60.4	12.9	2.0	0.2
	MPVSLFRRVWDYRDGEHETLESHYVVPQAALDRLFYSWFS	52.6	37.5	2.0	0.1

Figure 1A

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
<b>Design</b>	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R40-3-D5-IGFR	PLYGGGIHLYYPGTMGVPGFPRQVKVLGDADKNFYDWFPM	--	--	--	--	--
R40-3-A6-IGFR	YRGMVLVGRISDGAGKVASEP PARIGQKVFAVNFYDWFV	--	--	--	--	--
R40-X-R35-IGFR	SGCCRLLLGLRWMFIVVGWSGALVCQSAASAAGFYDWFV	--	--	--	--	--

**Figure 1B**

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20α-3-20D3-IR	IGGQGHQDGNFYDWFVEALA	46.3	36.2	7.0	5.2	0.2
R20α-3-20F1-IR	VFWNCRSQQLDFYEWFEQAA	49.0	26.0	2.8	9.3	0.1
R20α-3-20H1-IR	RVAGAISAPGLVSNKQDGLFYSWFRE	45.6	35.3	3.3	10.7	0.1
R20α-3-20D1-IR	VLQARHGCDVSDFYEWFA	50.8	37.5	3.0	12.5	0.1
R20β-4-B12-IR	GAFYRWFHEALVGSERVPDV	41.9	2.9	5.7	0.5	2.0
R20β-4-H3-IR	HEAFYDWFSAVDGGYELMG	13.9	5.8	2.4	2.4	0.4
R20β-4-D10-2-IR	RIGGGWARSEGIFYEWFVREL	21.5	7.3	2.9	2.5	0.4
R20β-4-C8-IR	LPAGGA?GFA?RGFYEWFES	44.9	31.1	9.6	3.2	0.3
R20β-4-E7-IR	GHSWALVRHVDRLFYEWFDL	45.0	18.8	5.9	3.2	0.3
R20β-4-E7-2-IR	LGTSAGQGVGHRAFYQWFQS	45.0	18.8	5.9	3.2	0.3
R20β-4-G3-IR	RGGGTFYEWFE <del>S</del> ALRKHGAG	38.6	7.5	2.0	3.8	0.3
R20β-4-H6-IR	NSSGQVVG <del>L</del> TFYSWFASQV	14.8	7.6	2.0	3.8	0.3
R20β-4-G11-IR	FYGWFSRQLSLTPRDDWG <del>L</del> P	39.4	7.5	1.9	3.9	0.3
R20β-4-G8-IR	RMFYEWFSQMAGPTEGSA	41.2	15.1	3.4	4.4	0.2
R20β-4-H9-IR	IGGQGHQDGNFYDWFVEALA	43.1	8.8	2.0	4.4	0.2
R20β-4-H8-IR	RDKPTDQEEQNWSFYEWFRH	47.9	43.7	9.3	4.7	0.2
R20β-4-B8-IR	WSALLSVMDTGFIYAWFDDAV	44.0	40.1	8.4	4.8	0.2
R20β-4-E2-IR	SRDQTNFTFNSAGFYGWFER	16.3	13.9	2.4	5.8	0.2
R20β-4-F4-IR	GVGTLTMSSDAFYTW <del>F</del> V	15.3	5.9	1.0	5.9	0.2
R20β-4-A8-IR	IGGSFVEFYGW <del>F</del> NDQV	43.3	36.0	6.0	6.0	0.2
R20β-4-C4-IR	DIGSDGHGRRWDSFYRW <del>F</del> EM	17.3	26.8	4.3	6.2	0.2
R20β-4-D7-IR	VLQARHGCDVSDFYEWFA	44.8	36.2	5.6	6.5	0.2
R20β-4-D2-IR	DPERMQSDVGFIYEW <del>F</del> RRAAVG	31.2	29.4	2.9	10.1	0.1

**Figure 1C**

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Design	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20-4-B9-IGFR	PERMQSDVGFYEWFRAAVG	40.1	16.6	--	--	--
R20-4-F8-IGFR	DIGSDGHGRRWDSFYRFEM	39.2	13.9	--	--	--
R20-4-G12-IGFR	PFYQWFLDQSVGSGRGGGLR	36.7	8.0	--	--	--
R20-4-D10-IGFR	AVAPLSVRGRDSGFYSWFSS	40.2	4.1	--	--	--

**Figure 1D**

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFSR	IR	IGFSR/IR	IR/IGFSR
A6S-3-E12-IR	XXXXXXXXXXNFYDWFVXXXX	26.2	1.3	8.0	0.2	6.2
A6S-2-C1-IR	GRVDWLQRNANFYDWFVAELG	41.2	1.3	7.0	0.2	5.4
A6S-1-A7-IR	RMFYSTGAPQNFYDWFVQEW	47.2	2.3	11.1	0.2	4.8
A6S-2-C8-IR	HHTQGLQVQRNFYDWFVNELR	44.9	1.5	5.5	0.3	3.7
A6S-3-E10-IR	MHRMQHDGTSNFYDWFVLQWA	46.9	1.6	5.0	0.3	3.1
A6S-2-D5-IR	AMHVVAQGGPNFYDWFVREL	31.9	1.2	3.7	0.3	3.1
A6S-1-B2-IR	AIQMNGLAFNFYDWFVRELT	31.6	1.8	5.3	0.3	2.9
A6S-1-A4-IR	TDRKSVQEPNRYDWFVWAAR	43.3	3.6	9.2	0.4	2.6
A6S-4-G3-IR	PHGHRGFAQSNFYDWFVTQEE	31.3	2.3	5.1	0.5	2.2
A6S-4-H8-IR	RLASASVPGQNFYDWFVDQLL	11.5	1.7	3.6	0.5	2.1
A6S-3-E11-IR	RQSEFSTLNSNFYDWFVRELE	26.3	2.3	4.4	0.5	1.9
A6S-1-A1-IR	GQAQLSIRDVNFYDWFVQQLV	36.9	3.7	6.5	0.6	1.8
A6S-2-C9-IR	MSEPAVGVNPNFYDWFVAQLF	43.6	1.3	2.3	0.6	1.8
A6S-2-C4-IR	VGTGRARLDNRYDWFVQGYS	34.5	5.6	9.6	0.6	1.7
A6S-4-H10-IR	SREAVQKRANFYDWFVQQLS	39.2	4.4	6.9	0.6	1.6
A6S-4-G7-IR	LAQFAGSRNQNFYDWFVEQLG	19.1	1.4	2.2	0.6	1.6
A6S-4-H2-IR	GQEIFDQMGLNFYDWFVRELD	25.5	2.6	3.9	0.7	1.5
A6S-2-C3-IR	RQPSQPPHGSNFYDWFVEAIN	31.1	1.6	2.4	0.7	1.5
A6S-2-C11-IR	LMQSLGSGSTNFYDWFVQQMV	20.9	3.3	4.6	0.7	1.4
A6S-3-F3-IR	DQORSACDGTNFYDWFVCQLS	37.1	3.0	4.2	0.7	1.4
A6S-3-E5-IR	LDGTKACQRVNFYDWFVCQTE	31.6	2.5	3.5	0.7	1.4
A6S-1-B7-IR	PEARRTVVHSNFYDWFVAQLS	49.2	1.6	2.3	0.7	1.4
A6S-3-E7-IR	PWMLSVGIQDNFYDWFVGLDS	37.2	5.0	6.3	0.8	1.3
A6S-4-G6-IR	ASHQORGGSSDNFYDWFVAQMR	16.8	3.1	4.0	0.8	1.3
A6S-2-C2-IR	TLEREGEFSGNFYDWFVEQLH	29.7	2.4	3.1	0.8	1.3
A6S-3-F1-IR	DRQSIGSVHGDYDWFVSALG	29.7	2.3	3.0	0.8	1.3
A6S-2-C5-IR	DWDKLGSLSENFYDWFVDQLA	42.9	6.1	7.0	0.9	1.1
A6S-3-E4-IR	VRVVLNQSGRNFYDWFVIOLE	20.9	2.1	2.3	0.9	1.1
	MASWQSRTPDNFYDWFVRELS					

Figure 1E

336263 " 33626363

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
A6S-3-E9-IR	TTCHPRGEDCNFYDWFVLQLR	36.6	9.0	8.9	1.0
A6S-3-E1-IR	VRGNDSVLRANFYDWFVDQLS	36.7	6.8	6.9	1.0
A6S-4-H12-IR	TPRSQVRSDHNFYDWFVYQLA	46.3	6.1	5.8	1.1
A6S-2-D3-IR	ESLTGSRPDRNFYDWFVQQT	37.0	5.3	5.1	1.0
A6S-3-E8-IR	PQSLTEVRTGNFYDWFVVQLH	42.7	5.2	5.1	1.0
A6S-1-A12-IR	DVGMRVKETNFYDWFVRQLI	39.7	2.1	2.1	1.0
A6S-4-H3-IR	GADDIRSLTNFYDWFVNQLS	18.6	3.1	2.9	1.1
A6S-3-F7-IR	GVSIIQAGYKTNFYDWFVEAVR	46.2	2.3	2.1	1.1
A6S-2-D8-IR	VGEHRQMSVGNFYDWFVMQIA	31.2	2.0	1.7	1.2
A6S-3-F10-IR	GSSSLGRSGPCNFYDWFVDQLE	39.0	5.9	4.5	1.3
A6S-4-G11-IR	HRQQDVVRQGNFYDWFVQALE	44.8	4.3	3.3	1.3
A6S-2-D2-IR	QDTFLTAREGNFYDWFIRALE	33.5	3.6	2.7	1.3
A6S-4-G8-IR	EAIMREEQANFYDWFVRQLE	11.1	2.5	1.9	1.3
A6S-4-H6-IR	VCDVSTGGTNFYDWFVCQVG	22.4	2.4	1.9	1.3
A6S-2-D10-IR	PQPRSASTPLNFYDWFVQATG	41.3	2.1	1.7	1.2
A6S-3-F4-IR	GVSRRGGDPNFYDWFVMQLR	37.0	13.5	9.9	1.4
A6S-4-G9-IR	GPGRHDSSRGNFYDWFVEQLA	36.2	11.8	7.8	1.5
A6S-3-F5-IR	ERFALEVQGSNFYDWFVRQVI	48.1	7.2	4.8	1.5
A6S-4-H1-IR	NLKSSATVGGNFYDWFVEQL	18.3	3.6	2.6	1.4
A6S-3-F6-IR	MEGPPAGGPLNFYDWFVAQVD	18.7	2.9	1.9	1.5
A6S-3-F11-IR	RLDVAGHRGGNFYDWFVKQLH	33.8	2.0	1.4	1.4
A6S-2-C6-IR	PWSDHEALNQNFYDWFVSQVL	46.7	19.2	12.1	1.6
A6S-4-G4-IR	EDRLNGESTNFYDWFVRQLA	36.9	18.2	10.7	1.7
A6S-4-G12-IR	GKLVASTLDDNFYDWFVRQLS	32.8	12.8	7.9	1.6
A6S-2-D7-IR	SGPVVQTQNGNFYDWFVHQLR	33.2	12.0	7.1	1.7
A6S-4-G10-IR	VDRAGPAGSDNFYDWFVAQLD	33.9	10.8	6.8	1.6
A6S-3-F9-IR	SLGRNDRPDENFYDWFVSQVQ	44.3	9.6	5.7	1.7
A6S-3-F2-IR	RVMATANAPMNFYDWFVVQLQ	23.2	4.3	2.5	1.7

Figure 1E (Con't)

Clone	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
<b>Design</b>	XXXXXXXXXXNFYDWFVXXXX	--	--	--	--	--	
A6S-4-G1-IR	NGVERAGTGDNFYDWFVAQLH	36.2	31.8	15.7	2.0	0.5	
A6S-1-A3-IR	PFAGKGDKTGNFYDWFVSLTG	39.9	12.6	6.0	2.1	0.5	
A6S-3-F12-IR	GMPQEYMDQVNFYDWFVAQVD	41.4	7.4	4.0	1.9	0.5	
A6S-4-G2-IR	MGTPAVGDGANFYDWFVRQLG	26.7	7.0	3.5	2.0	0.5	
A6S-1-B1-IR	SKCKAWYGANNFYDWFVWQVD	30.6	3.7	1.9	1.9	0.5	
A6S-2-D11-IR	EAASLGSQDRNFYDWFVRQVV	48.4	37.4	13.5	2.8	0.4	
A6S-2-D1-IR	VERSASSQDGNFYDWFVVQIR	37.8	30.6	12.0	2.6	0.4	
A6S-3-E2-IR	TSEVQRRSQDNFYDWFVAQVA	33.1	24.7	9.8	2.5	0.4	

**Figure 1E (Con't)**

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
A6S-4-E4-IGFR	XXXXXXXXXXNFYDWFVXXXX	--	--	--	--
A6S-2-D2-IGFR	ERSAAGFREGNFYDWFVAQVN	27	32	--	--
A6S-2-F2-IGFR	RAERGSMDNSNFYDWFVQQLP	36	30	--	--
A6S-4-F3-IGFR	LAMSVASRPANFYDWFVAQIV	35	30	--	--
A6S-4-G4-IGFR	HNSSSPMRTGNFYDWFVQELR	26	30	--	--
A6S-4-G3-IGFR	SALSGPVQPINFYDWFVTGM	26	30	--	--
A6S-2-H2-IGFR	GAQAIREIHNFYDWFVAQVT	21	29	--	--
A6S-2-E3-IGFR	RQRESDSGTNFYDWFVGAIR	40	28	--	--
A6S-4-C6-IGFR	VQEGLSGMEGNFYDWFVDQLF	36	28	--	--
A6S-4-F5-IGFR	RLDRSSTSGVNFYDWFVAQVG	25	28	--	--
A6S-4-H3-IGFR	GSQHSGREPHNFYDWFVAQVG	24	28	--	--
A6S-4-H4-IGFR	GRGDQRHETTNFYDWFVRELQ	20	28	--	--
A6S-2-H1-IGFR	PRMVEKPSEDNFYDWFVTQLS	20	28	--	--
A6S-4-E6-IGFR	RVGIQVDPHTNFYDWFVIQLT	42	27	--	--
A6S-4-B6-IGFR	RSSGGLLSQGNFYDWFVSQLE	24	26	--	--
A6S-4-D2-IGFR	SDARQAGLQENFYDWFVSQVR	23	26	--	--
A6S-4-G5-IGFR	PYRSSLGENFYDWFVMQVR	19	26	--	--
A6S-2-A3-IGFR	QEVTRTRDDKNFYDWFVSQIF	18	26	--	--
A6S-4-E2-IGFR	SRAPYGSTAGNFYDWFVQAVS	37	25	--	--
A6S-4-G2-IGFR	?DGQSVSSKGNFYDWFVQQMT	25	25	--	--
A6S-4-D6-IGFR	RLMGGIAEPQNFYDWFVREVA	20	25	--	--
A6S-4-F4-IGFR	SAGHHMPRESNFYDWFVKQVS	25	24	--	--
A6S-4-C3-IGFR	LGAETWDGINFYDWFVKQVS	22	24	--	--
A6S-4-H5-IGFR	VHSGVPPYPNFYDWFVMQVS	22	24	--	--
A6S-4-H6-IGFR	VTMLDKGAQDNFYDWFVREVA	21	24	--	--
A6S-4-F6-IGFR	HHSPGNEHGYNFYDWFVLQVA	19	24	--	--
A6S-3-H1-IGFR	GSIAQLIMRANFYDWFVEQTN	18	24	--	--
	LKGSSQPLSVNFYDWFVQQIK	17	24	--	--
	PASNKNSLAENFYDWFVQQTR	30	23	--	--

Figure 1F





[illegible]

**Figure 1F (Con't)**

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
A6L-3-D1-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV	19.0	.4.0	--	--	--
A6L-4-H7-IR		QRGMLVRGRISHGAGKIAIEPPDCLGQKACAVNFYDWFV	22.6	19.8	26.5	0.7	1.3
A6L-4-H4-IR		QRGMLLLGRISDDAGKVASEPSARRGQKVFAFNFYDWFV	37.5	3.5	4.2	0.8	1.2
A6L-4-E4-IR		YRGILVLGRISSEGAGKVASEPARIGQKVFAFNFYDWFV	38.5	21.1	25.8	0.8	1.2
A6L-4-G7-IR		QRGMLALGRISDGAGKVASEPPAGIGQKVFAFNFYDWFV	38.1	5.4	6.0	0.9	1.1
A6L-3-C3-IR		FRGRLVLGHFSDGAGKVSEPARIGQKVFDVNFYDWFV	38.6	16.2	18.5	0.9	1.1
A6L-3-B6-IR		YRGMLVLGRISDGAGKVASEPARIGQEVFADNFYDWFV	34.7	21.8	23.1	0.9	1.1
A6L-4-G11-IR		YRGMLVLGRISDGAGEVASEPARIGQEVFALNFYDWFV	33.1	27.8	30.3	0.9	1.1
A6L-4-G12-IR		VPWYAGSGSSSDGAGKVASEPPARIDQKVFAVNFYDWFV	27.6	2.0	2.0	1.0	1.0
A6L-3-A10-IR		YRGQLVLGRISYGAGKVGCDPPARIGQKDWAVNFYDWFV	32.0	2.3	2.3	1.0	1.0
A6L-4-E12-IR		QRGLLVLGRFSDGAGNVASEPPAGIGQEVFPVNFYDWFV	21.1	2.4	2.4	1.0	1.0
A6L-4-E10-IR		QRGMLVLGRISDGAGKVAEPPDCLGQKVCANFYDWFV	3.1	2.4	2.4	1.0	1.0
A6L-4-G8-IR		QRGMRVLGRISDGAGKVAEPPRIGQKDFAVNFYDWFV	30.1	3.8	3.8	1.0	1.0
A6L-3-C12-IR		QPGWAGSGRIYDGAGKVASEPPAHIGQEVFAVNFYDWFV	37.9	4.7	4.7	1.0	1.0
A6L-4-H11-IR		QRGMLVLDRISDGAGKVASEPPARIGQNVAVNFYDWFV	29.5	5.7	5.7	1.0	1.0
A6L-4-F10-IR		YRGMLVWGRISDGTGKVASQPPARIGQKVFAVNFYDWFV	35.4	9.6	9.6	1.0	1.0
A6L-4-E9-IR		YRGMLVLGRISDGAGKVASEPPAHIGQKVFAFNFYDWFV	31.6	10.5	10.5	1.0	1.0
A6L-4-H8-IR		QHGMLVLGRVSVGAGKVPSEPPAHIGKVFADNFYDWFV	39.8	12.9	12.9	1.0	1.0
A6L-3-A11-IR		YSGYAGSGSFDGAGKVASEPPARISQEVADNFYDWFV	38.2	14.6	14.6	1.0	1.0
A6L-4-F9-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVSANFYDWFV	29.0	17.5	17.5	1.0	1.0
A6L-4-G2-IR		YHGKLDLGRISVGVGKVASEPPARIGQKVFAFNFYDWFV	35.7	18.4	18.4	1.0	1.0
A6L-4-E8-IR		YRGQAGSGVSLTVAGKVADPPARIGQKVFAFNFYDWFV	29.5	21.4	20.7	1.0	1.0
A6L-4-H10-IR		HRGMLVLGRISDGAGNVDPPEPPARIGQNVFAGNFYDWFV	28.7	21.6	21.6	1.0	1.0
A6L-4-G9-IR		QRGMPVLGRISDGAGKVGSEPPARIARKVFPVNFYDWFV	30.0	22.1	22.1	1.0	1.0
A6L-4-F7-IR		QGGLLVTGRISDGAGKVASEPPGGIGQKVFAFNFYDWFV	37.1	22.6	22.6	1.0	1.0
A6L-4-E11-IR		YPWYGGSGTYLDGAGKVASEPPARIDQQVFAGNFYDWFV	28.6	23.6	24.4	1.0	1.0
			38.4	26.5	26.5	1.0	1.0

Figure 1C



Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		YRGMLVLGRISDGAGKVASSEPPARIGQKVFAVNFYDWFV	19	4	--	--	--
	A6L-4-F8-IGFR	YRGMMVQGRISDGAGKVASVPRIGQKVI AVNFYDWFV	26	28	--	--	--
	A6L-2-G9-IGFR	YRGRLGLGRISDVAGKVACDPSARIGQKVL PVNFYDWFV	39	22	--	--	--
	A6L-4-E7-IGFR	YRGMLVLGRISDGAGRVASEPQARIGQKVFAVNFYDWFV	23	22	--	--	--
	A6L-4-G10-IGFR	QGGMLVPGRISDGAGKVASQPPARIGPKGFAGNFYDWFV	19	22	--	--	--
	A6L-2-E9-IGFR	YRGMRVLGRISDGAGKVASSEPTTHIGQKVFPVNFYDWFV	38	21	--	--	--
	A6L-2-D6-IGFR	YRGMLVLGRISDGAGKVGSEPAARIGQKVFAVNFYDWFV	34	21	--	--	--
	A6L-3-H12-IGFR	YRGQGMVLGRISDGAGKVASSEPPGRIGQKVFPVNFYDWFV	24	21	--	--	--
	A6L-4-A7-IGFR	YRGMVLGRITGGAGKVASSEPPDRIGQHVFVDNFYDWFV	20	20	--	--	--
	A6L-4-B8-IGFR	DGMLVLGRISDGAGNVASEAPARIGQKVFAVNFYDWFV	20	19	--	--	--
	A6L-4-G7-IGFR	YRGMVRGRISDGAGKAA SDPRARIGQTVLDVNFYDWFV	19	19	--	--	--
	A6L-2-D9-IGFR	YRGMWVLGRISYGAGKVAYEPPARMGQKGFAVNFYDWFV	38	18	--	--	--
	A6L-4-F7-IGFR	YRGMVLGGRIAGGAGIVASEPPARIGQKVFAVNFYDWFV	18	18	--	--	--
	A6L-4-E12-IGFR	YRGLLGLGGRISDGAGKVASSEPPARNQKVFAVNFYDWFV	15	13	--	--	--
	A6L-4-H7-IGFR	YRGMVLGRISAGAGKVASGAPARIGQEDFAVNFYDWFV	14	13	--	--	--
	A6L-4-H12-IGFR	YRGMALGRISSEGAGKVASSEPPARIGQNVFAVNFYDWFV	13	12	--	--	--
	A6L-2-A4-IGFR	YRGMVLGRISDGAGKVASSEPPARIGQKVLAVNFYDWFV	17	4	--	--	--
	A6L-3-D10-IGFR	YPGMLVPGRISDGAGEGATDPPPRIGQKVFAFNFYDWFV	16	4	--	--	--
	A6L-2-F6-IGFR	YRGMVLPGRISDGAGKVAYEPPARIGQKIFAVNFYDWFV	15	4	--	--	--
	A6L-2-B11-IGFR	YRGVLVLRVSDGVGKVASSEPPAHRGQRVFGVNFYDWFV	26	3	--	--	--
	A6L-1-B7-IGFR	YRRMLVLGRISDGAANVASGPPDRIGQKVFAVNFYDWFV	23	3	--	--	--
	A6L-1-D8-IGFR	YRRMALGRFSDVTGDVASEPPAHIGQKVVAVNFYDWFV	23	3	--	--	--
	A6L-0-A11-IGFR	YRGMVVRGRIFDGPVKVASEPRARIGQKVFAVNFYDWFV	19	3	--	--	--
	A6L-3-B7-IGFR	YRGMVLGRISDGAGKVASSEPPARVGDVVAVNFYDWFV	9	3	--	--	--
	A6L-1-G7-IGFR	YPGRLVGGRISDGVGKVASSEPPGRIGQKVFAVNFYDWFV	20	2	--	--	--
	A6L-1-B9-IGFR	QRGLLVLGRIFDAGKVASDPPPARIGQKDFADNFYDWFV	18	2	--	--	--
	A6L-1-C9-IGFR	YRGMVLGRISDGAGKVAFEP PARIGQNVFAVNFYDWFV	18	2	--	--	--
	A6L-0-G10-IGFR	YRCMPVLGRISDGAG#VASDRPARIGQKVFAVNFYDWFV	18	2	--	--	--
	A6L-1-G8-IGFR	YRGLVLGRISDGAGKVA AEPPASMDSKVFAGNFYDWFV	15	2	--	--	--

### Figure 1H

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	GFREGNFYDWFVAQVT	--	--	--	--	--
E4Dα-1-B8-IR	GFREGQRYWVFVAQVT	40.7	1.0	12.3	0.1	12.3
E4Dα-3-E5-IR	GFREGYFYDWFVAQVT	39.6	2.0	1.5	1.3	0.8
E4Dα-1-A1-IR	GFREGDFYEWVFVAQVT	48.7	44.9	31.4	1.4	0.7
E4Dα-2-D9-IR	GFREGQFYEWFAAQVT	22.9	3.3	2.4	1.4	0.7
E4Dα-1-B3-IR	GFREGTFYDWFVAQVT	41.8	38.6	26.5	1.5	0.7
E4Dα-1-A6-IR	GFREGNFYDWFVAQVT	56.3	51.2	32.6	1.6	0.6
E4Dα-1-A10-IR	GFREGAFYDWFVAQVT	48.9	42.2	26.5	1.6	0.6
E4Dα-1-A8-IR	GFREGAFYDWFVAQVT	46.9	41.5	26.2	1.6	0.6
E4Dα-1-B1-IR	GFREGKFYQWFEAQVT	44.1	31.1	19.7	1.6	0.6
E4Dα-2-C9-IR	GFREGDFYDWFVAQVT	34.0	8.1	4.8	1.7	0.6
E4Dα-1-A3-IR	GFREGTFYEWVFVAQVT	45.3	40.3	22.5	1.8	0.6
E4Dα-1-A9-IR	GFREGNFYDWFVAQVT	46.9	41.0	22.5	1.8	0.5
E4Dα-3-F3-IR	GFREGQFYEWFLAQVT	37.2	14.1	8.0	1.8	0.6
E4Dα-2-D3-IR	GFREGQFYDWFVAQVT	35.1	16.3	8.7	1.9	0.5
E4Dα-2-D6-IR	GFREGDFYDWFVAQVT	33.2	5.6	2.8	2.0	0.5
E4Dα-3-F10-IR	GFREGQFYDWFVAQVT	27.8	4.5	2.3	2.0	0.5
E4Dα-2-D5-IR	GFREGYFYEWVFVAQVT	43.8	23.8	11.4	2.1	0.5
E4Dα-3-F4-IR	GFREGDFYQWFEAQVT	25.9	7.6	3.7	2.1	0.5
E4Dα-3-E3-IR	GFREGSFYGFVAQVT	34.6	4.0	1.9	2.1	0.5
E4Dα-3-F8-IR	GFREGSFYAWFVAQVT	20.9	16.0	7.4	2.2	0.5
E4Dα-2-C1-IR	GFREGQFYDWFVAQVT	43.1	11.6	5.0	2.3	0.4
E4Dα-1-B4-IR	GFREGIFYEWVFVAQVT	45.3	6.6	2.9	2.3	0.4

Figure 1I

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
	GFREGNFYDWFVAQVT	--	--	--	--
E4D $\alpha$ -4-H5-IR	GFREGSFYEWFOAQVT	47.2	36.0	2.4	0.4
E4D $\alpha$ -1-B12-IR	GFREGNFYDWFVAQVT	47.6	33.4	2.4	0.4
E4D $\alpha$ -4-G2-IR	GFREGSFYDWFVAQVT	23.4	20.4	2.4	0.4
E4D $\alpha$ -3-F9-IR	GFREGDFYDWFVAQVT	36.2	15.6	2.5	0.4
E4D $\alpha$ -4-G6-IR	GFREGDFYQWFVAQVT	26.0	4.9	2.5	0.4
E4D $\alpha$ -4-H9-IR	GFREGGFYDWFVAQVT	47.8	24.8	2.6	0.4
E4D $\alpha$ -2-C10-IR	GFREGDFYDWFVAQVT	42.4	23.2	2.6	0.4
E4D $\alpha$ -1-B2-IR	GFREGVFYDWFVAQVT	39.4	18.7	2.6	0.4
E4D $\alpha$ -3-F12-IR	GFREGGFYEWFOAQVT	38.9	16.6	3.0	0.3
E4D $\alpha$ -2-D11-IR	GFREGSFYDWFVAQVT	40.2	11.1	3.4	0.3
E4D $\alpha$ -4-H2-IR	GFREGNFYEWFOAQVT	37.8	33.9	4.1	0.2
E4D $\beta$ -4-A12-IR	GFREGKFYDWFVAQVT	41.1	8.3	0.3	3.5
E4D $\beta$ -4-A10-IR	GFREGGFYEWFOAQVT	5.8	1.2	2.4	2.0
E4D $\beta$ -4-E10-IR	GFREGVFYDWFVAQVT	9.6	1.2	2.2	1.8
E4D $\beta$ -4-B11-IR	GFREGTFYDWFVAQVT	36.1	15.2	0.6	1.8
E4D $\beta$ -4-C10-IR	GFREGGFYEWFOAQVT	27.8	13.3	0.6	1.7
E4D $\beta$ -4-E8-IR	GFREGDFYEWFEAQVT	28.7	16.7	0.6	1.7
E4D $\beta$ -4-G7-IR	GFREGHFYDWF?AQVT	30.9	14.7	0.6	1.5
E4D $\beta$ -4-C8-IR	GFREGGFYDWFVAQVT	35.5	22.5	0.7	1.5
E4D $\beta$ -4-A8-IR	GFREGSFYDWFVAQVT	31.2	14.5	0.7	1.5
E4D $\beta$ -4-A9-IR	GFREGSFYDWFVAQVT	35.8	9.0	0.7	1.4
E4D $\beta$ -4-G11-IR	GFREGTFYDWFVAQVT	28.9	9.7	0.7	1.4
E4D $\beta$ -4-B9-IR	GFREGNFYEWFTAQVT	27.2	9.1	0.7	1.4
E4D $\beta$ -4-F10-IR	GFREGSFYNWFVAQVT	7.7	1.5	0.7	1.3
E4D $\beta$ -4-D12-IR	GFREGNFYDWFVAQVT	41.1	27.2	0.8	1.3
E4D $\beta$ -4-B8-IR	GFREGDFYDWFVAQVT	35.9	27.0	0.8	1.3
E4D $\beta$ -4-G10-IR	GFREGAFYDWFVAQVT	38.5	25.5	0.8	1.3

Figure 11 (Con't)

# CONFIDENTIAL

E4Dβ-4-D9-IR	GFREGSFYDWFEEAQVT	34.1	19.3	25.7	0.8	1.3
E4Dβ-4-F8-IR	GFREGSFYDWFEEAQVT	39.3	35.6	44.4	0.8	1.2
E4Dβ-4-E12-IR	GFREGSFYEWFDAAQVT	40.2	27.8	33.4	0.8	1.2
E4Dβ-4-H12-IR	GFREGAFYDWFEEAQVT	41.2	27.1	32.3	0.8	1.2
E4Dβ-4-C9-IR	GFREGQFYDWFEEAQVT	38.0	22.5	27.6	0.8	1.2
E4D -4-H9-IR	GFREGNFYDWFEEAQVT	38.7	33.3	36.6	0.9	1.1
E4D -4-G9-IR	GFREGDFYDWFEEAQVT	10.9	4.9	5.6	0.9	1.1
E4Dβ-4-F12-IR	GFREGSFYEWFEAQVT	14.8	5.9	6.1	1.0	1.0
E4Dβ-4-F9-IR	GFREGGFYDWFEEAQVT	39.3	31.3	28.3	1.1	0.9
E4Dβ-4-F7-IR	GFREGGFYAWFEAQVT	31.0	22.2	19.5	1.1	0.9
E4Dβ-4-B7-IR	GFREGGFYEWFAQVT	--	--	--	--	--

Figure 1I (Con't)



Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
E4D-2-E7-IGFR	GFREGNFYDWFVAQVT	--	--	--	--	--
E4D-2-C11-IGFR	GFREGDFYDWFRAQVT	20.8	22.8	--	--	--
E4D-2-B1-IGFR	GFREGSFYDWFVAQVT	21.5	22.6	--	--	--
E4D-2-D10-IGFR	GFREGDFYDWFVAQVT	22.0	22.5	--	--	--
E4D-2-A9-IGFR	GFREGGFYDWFVAQVT	20.6	22.1	--	--	--
E4D-2-E5-IGFR	GFREGDFYDWFVAQVT	17.4	21.5	--	--	--
E4D-2-H9-IGFR	GFREGDFYDWFVAQVT	24.2	21.2	--	--	--
E4D-1B-C4-IGFR	GFREGGFYDWFVAQVT	19.1	20.7	--	--	--
E4D-2-E10-IGFR	GFREGDFYDWFVAQVT	24.3	20.5	--	--	--
E4D-2-F4-IGFR	GFREGNFYDWFVAQVT	21.0	20.5	--	--	--
E4D-2-C10-IGFR	GFREGNFYDWFVAQVT	25.0	20.2	--	--	--
E4D-3-D8-IGFR	GFREGHFYDWFVAQVT	22.8	20.1	--	--	--
E4D-3-F9-IGFR	GFREGQFYDWFVAQVT	21.1	19.8	--	--	--
E4D-1B-E5-IGFR	GFREGSFYDWFVAQVT	22.6	19.7	--	--	--
E4D-2-F3-IGFR	GFREGDFYDWFVAQVT	24.2	18.8	--	--	--
E4D-3-D5-IGFR	GFREGHFYDWFVAQVT	23.6	18.0	--	--	--
E4D-3-G10-IGFR	GFREGQFYDWFVAQVT	22.2	18.0	--	--	--
E4D-2-F6-IGFR	GFREGQFYDWFVAQVT	22.1	17.6	--	--	--
E4D-2-F7-IGFR	GFREGQFYDWFVAQVT	24.6	17.5	--	--	--
E4D-3-B7-IGFR	GFREGDFYDWFVAQVT	19.0	17.5	--	--	--
E4D-1B-C12-IGFR	GFREGNFYDWFVAQVT	23.0	16.4	--	--	--
E4D-3-B1-IGFR	GFREGSFYDWFVAQVT	23.0	16.1	--	--	--
E4D-2-E2-IGFR	GFREGHFYDWFVAQVT	21.6	16.0	--	--	--
E4D-2-D1-IGFR	GFREGDFYDWFVAQVT	21.9	14.1	--	--	--
E4D-1-D4-IGFR	GFREGHFYDWFVAQVT	24.5	13.2	--	--	--
E4D-1B-A10-IGFR	GFREGYFYDWFVAQVT	18.9	12.4	--	--	--
E4D-1B-A3-IGFR	GFREGHFYDWFVAQVT	23.9	10.8	--	--	--
E4D-1-B5-IGFR	GFREGDFYDWFVAQVT	22.2	10.8	--	--	--
	GFREGTFYDWFVAQVT	19.0	10.8	--	--	--

Figure 1J

Clone	Sequence	Ratios over Background		Comparisons	
D sign		E-Tag	IGFsR	IGFR/IR	IR/IGFR
E4D-1B-B8-IGFR	GFREGNFYDWFVAQVT	--	--	--	--
E4D-1-G7-IGFR	GFREGDYWGFEAQVT	23.8	10.7	--	--
E4D-1B-A11-IGFR	GFREGDFYAWFMAQVT	14.3	10.5	--	--
E4D-1-C3-IGFR	GFREGNFYEWFLAQVT	24.0	10.0	--	--
E4D-2-H1-IGFR	GFREGSFYDWFDAQVT	15.8	9.3	--	--
E4D-1-C2-IGFR	GFREGNFYDQFVAQVT	19.6	4.9	--	--
E4D-1B-A12-IGFR	GFREGHFYEWFAAQVT	11.5	4.5	--	--
E4D-1B-A1-IGFR	GFREGKFYDWFVAQVT	18.4	3.5	--	--
E4D-2-A3-IGFR	GFREGMFDVQLLAQVT	22.5	2.9	--	--
		22.7	2.1	--	--

Figure 1J (Con't)

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR
Design	XXXXXXXXFHENFYDWFVRQVSXXXXXX	--	--	--	--
Parental	VTFTSAVFHENFYDWFVRQVS	29.8	17.5	16.3	1.1
	TYKARFLHENFYDWFNRQVSQYFGRV	37.7	2.2	18.1	0.1
H2CA-4-F11-IR	QRLSLHEQFYDWFVGQVSPLGAGG	31.2	4.4	18.8	0.2
H2CA-4-E10-IR	GGKVNFDHEDFYGWFVQQFSGVGSDDR	36.1	13.4	25.7	0.5
H2CA-4-G3-IR	LVGDAPFHEDFYDWFARQVFGCCQEQ	35.6	12.1	22.0	0.5
H2CA-3-A11-IR	TGAEVSFHENFYDWFDRQYSSWLDRD	36.0	21.1	33.5	0.6
H2CA-4-F8-IR	QPHSSRLHESFYDWFDRQVPWYALDR	37.1	23.3	34.3	0.7
H2CA-4-G4-IR	SRALAAVHEQFYDWFVRQVSGLDWGY	39.8	25.0	35.6	0.7
H2CA-4-F4-IR	QPKDGLTHENFYDWFVRQVSSGWVG	33.5	5.1	6.6	0.8
H2CA-4-H10-IR	RGRLIQLHEDFYDWFRLRQVSGMGGS	36.1	19.6	25.1	0.8
H2CA-4-F1-IR	QRGAPKSDENFYDWFVRQVLRFGEND	39.3	24.3	31.9	0.8
H2CA-3-D5-IR	AARTSLFHEDFYEWFDQRVRQEGMWG	8.2	2.6	3.2	0.8
H2CA-4-E11-IR	GTSNHSLSHENFYDWFVRQLSSVQSSG	35.9	9.9	12.1	0.8
H2CA-3-B6-IR	VSHVHLFHENFYDWFVRQLAAEGFSG	37.3	30.1	36.2	0.8
H2CA-3-A9-IR	GRQDSGLHEHYDWFVRQVQGEVALG	38.6	35.4	37.3	1.0
H2CA-4-H5-IR	SNDERQFHETFYDWFVRQVSADGADR	29.3	5.1	5.6	0.9
H2CA-3-C9-IR	LSTEQRFHKEFYDWFVHVQVSTSGGT	37.2	16.9	19.1	0.9
H2CA-3-A10-IR	SLSRQFHENFYDWFARQVSELEGVV	29.2	28.6	32.2	0.9
H2CA-3-A3-IR	IPGRRSLHENFYDWFVRQVSPGGGSA	32.4	29.1	31.6	0.9
H2CA-4-G8-IR	TQKAQSLDEKFYDWFVRQVSGGLTG	36.1	34.4	36.4	0.9
H2CA-4-G9-IR	VSQLSDFHENFYGWFARQIAGQAEWT	34.2	35.5	37.7	0.9
H2CA-4-G10-IR	NGTSQALHQNFYDWFQAQISGSEPGP	37.0	36.0	40.0	0.9
H2CA-4-H7-IR	VGQSVTFHGDFYDWFDRQLSGSQEFG	37.5	36.7	39.5	0.9
H2CA-4-F9-IR	TIDHPLHEQFYDWFARQVSDLES LG	37.7	37.6	39.9	0.9
H2CA-4-F7-IR	PNVGYAFHENFYDWFIRQVSIIEKAG	18.7	3.6	3.5	1.0
H2CA-3-D10-IR	SRGSGVFHESFYNWFDRQVSEW IQFG	26.5	21.4	21.5	1.0
H2CA-3-B1-IR	QPVSGSVHERFYDWFVRQVSGSAGGG	32.9	22.9	22.4	1.0
H2CA-3-A5-IR	ASQLPPVYENFYEWFDQRVSLDAQRE	26.6	27.7	28.5	1.0
H2CA-4-F10-IR					

### Figure 1K (Con't)

1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 26

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGfsR	IR	IGFR/IR	IR/IGFR
H2CA-3-D12-IR	XXXXXXXXFHENFYDFWFRVQVSGXXXXX	--	--	29.6	--	--
H2CA-3-B5-IR	SEDDSRHENFYDFWFRVQVSGICLQD	36.8	34.1	29.6	1.2	0.9
H2CA-4-1-IR	PAPADAFDHNFYDFWFRQJLSATTITQ	38.8	35.2	30.5	1.2	0.9
H2CA-3-D3-IR	MVQRISIHENFYDFWFRQJLSGSVAPP	29.8	12.5	11.3	1.1	0.9
H2CA-4-E3-IR	GNVRGQFHGFYDFWFRQVSGSEGDA	33.1	29.9	27.5	1.1	0.9
H2CA-4-E12-IR	PDAXQFHETHFYGMFVRQJLSEDSAMS	33.3	32.3	30.2	1.1	0.9
H2CA-3-A6-IR	FCRGVHCDENFYDFWFRQVSGALLGEG	36.0	32.4	29.4	1.1	0.9
H2CA-4-E9-IR	ETPLTELHEQFYDFWFRVQVSGPFGV	34.0	33.1	30.6	1.1	0.9
H2CA-4-F3-IR	QHRGPHFHEFYDFWFRVQVSSAPSD	38.8	33.7	29.7	1.1	0.9
H2CA-4-H6-IR	RODPGLFHDNFYDFWFRDLVLSAMDGE	41.0	34.2	32.0	1.1	0.9
H2CA-4-H2-IR	QAAVGVCKNOFYAMFACQVREDFAKA	37.1	34.5	30.8	1.1	0.9
H2CA-3-D4-IR	RSEQYRFHENFYEHFDRQVSRWGLLG	41.8	35.3	32.8	1.1	0.9
H2CA-3-D1-IR	RWNVLQFNENFYDFDRQVSAIRGGG	38.7	35.5	32.3	1.1	0.9
H2CA-3-C1-IR	GAGGRDFDEFYDFWFRQJLSSTVSGT	34.5	35.5	31.3	1.1	0.9
H2CA-3-D8-IR	SPGKLVHDQFYDFWFRQJLSSTAGT	39.9	36.1	32.9	1.1	0.9
H2CA-4-H4-IR	QGGGLGDFDEFYDFWFRQVSRDRRAD	37.8	36.7	33.1	1.1	0.9
H2CA-4-P6-IR	LSQGVGFQENFYEFWRQVSGWDGRD	38.5	37.0	33.7	1.1	0.9
H2CA-4-B4-IR	VFRSRCHDNFYDFWFFQVSGQADGG	38.7	37.5	35.2	1.1	0.9
H2CA-3-C11-IR	LLASRAFHENFYDFWFRQVSGTQPPG	38.6	38.0	34.7	1.1	0.9
H2CA-4-E6-IR	VPDQIQI FHESFYDFWFRQASAGGPAD	40.3	38.3	36.1	1.1	0.9
H2CA-3-D7-IR	ANQMKGRFHDNFYDFWFRQVSRVERGT	41.9	38.4	35.0	1.1	0.9
H2CA-4-G12-IR	PSRKDGLHQSFYDFWFRQVDMEGRA	39.3	38.8	35.8	1.1	0.9
H2CA-3-D6-IR	QAVTRRFHENFYDFWFRQVSEEGGWS	42.5	39.2	35.5	1.1	0.9
H2CA-4-H12-IR	GVAVGQYQANFYDFWFRQVDMGNSGG	35.3	15.2	11.6	1.3	0.8
H2CA-3-D11-IR	GHQRDLHESFYDFWFRVQVSEAGGG	37.6	19.4	15.1	1.3	0.8
H2CA-3-C12-IR	DRPSSFIFHENFYEFWFRQVSGSSGG	39.4	36.2	27.6	1.3	0.8
H2CA-3-D1-IR	ERTAEITLHEQFYDFWFRQVSMADGES	40.0	38.4	29.3	1.3	0.8
H2CA-3-D11-IR	LTSQULLSHEDFYDFWFRQVSGVGGG	38.1	32.9	27.2	1.2	0.8
H2CA-3-C12-IR	PQRSRDLRDDNFYDFWFRQVSGVONED	38.5	38.4	31.7	1.2	0.8

### Figure 1K (Con't)

# Table 3C.2

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXHNFYDWFVRQVXXXXXXXX	--	--	--	--	--
H2CA-4-G7-IR	RAGGVGLHDNFYDWFVRQVSGDSDGP	35.9	34.7	23.7	1.5	0.7
H2CA-3-C6-IR	ADCYVQLHNFYDWFRRQVCNLQEGM	38.7	37.6	28.2	1.3	0.7
H2CA-3-B8-IR	ROGHAGFHDNFYDWFVRQVSGSTPQV	37.8	19.6	9.9	2.0	0.5

Figure 1K (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Parental	XXXXXXXXHNFYDFWFRQVSXXXXXX	--	--	--	--	--
H2CA-4-G9-IGFR	VTFTSAVFHENFYDFWFRQVS	29.8	17.5	16.3	1.1	0.9
H2CA-4-H6-IGFR	GIISQSCPESFYDFWFPAGQVSDPWWCW	8.6	9.5	0.6	16.0	0.1
H2CA-4-F-IGFR5	VGRASGFPENFYDFWFRQLSLQSGEQ	4.9	10.5	0.7	14.6	0.1
H2CA-4-H8-IGFR	VGYQGQDENFYDFWFRQVSGRLGVQ	5.5	9.7	0.8	12.3	0.1
H2CA-4-F11-IGFR	SACQDFCHENFYDFWFRQVSGGAAYG	5.6	9.2	1.0	9.4	0.1
H2CA-4-F6-IGFR	SAAQLFFQESFYDFWFLRQVAESSQPN	3.5	6.8	1.0	6.7	0.1
H2CA-4-F10-IGFR	AVRATRFDEAFYDFWFRQISDGQGNK	3.9	7.3	1.1	6.4	0.2
H2CA-1-A3-IGFR	VNQSGSIHENFYDFWFRQVSHQRGVR	4.9	5.7	1.0	5.9	0.2
H2CA-3-C8-IGFR	APDPDFQEIFYDFWFRQVSRMPGGG	7.7	3.8	0.8	5.1	0.2
H2CA-2-B9-IGFR	SSCDGAGHESFYEWFRQVSGCRSV	15.1	5.6	1.2	4.8	0.2
H2CA-4-H4-IGFR	RAGSSDFHEDFYEWFRQVLSLKGK	9.3	7.0	1.7	4.2	0.2
H2CA-4-F7-IGFR	QAVQPGFHEEFYDFWFRQVSTGVGGG	3.9	4.1	1.0	4.2	0.2
H2CA-3-D6-IGFR	SSIGGFHENFYDFWFRQLSQSPPLK	1.5	3.2	0.8	4.1	0.2
H2CA-3-D8-IGFR	QSPVGSSHEDFYDFWFRQVQAQSGAHQ	8.3	9.0	2.2	4.0	0.3
H2CA-4-G11-IGFR	NYRRQVFNNGFYDFWFRQVFSLVTPG	10.9	7.2	1.8	4.0	0.3
H2CA-4-F1-IGFR	TLDGGSFEEQFYDFWFRQLSYRTNPD	10.8	9.5	2.5	3.9	0.3
H2CA-3-D7-IGFR	FYVQWGHENFYDFWFRQVSGGAG	5.8	3.5	0.9	3.8	0.3
H2CA-1-A7-IGFR	LRRQAPVEENFYDFWFRQVSGDRVGG	13.3	3.0	0.8	3.7	0.3
H2CA-2-B4-IGFR	RCGRELYHSTFYDFWFRQVAGRTCPS	8.0	2.2	0.6	3.7	0.3
H2CA-2-B3-IGFR	CCLLCRFQQNFYDFWFRVCQGISRLRPL	3.5	4.1	1.1	3.6	0.3
H2CA-2-B2-IGFR	PPLASDLDVQFYGWFRVQVSPPPGRGG	7.7	3.8	1.0	3.6	0.3
H2CA-3-D4-IGFR	GAPVDQLHEDFYDFWFRQVQAATG	4.1	3.4	1.0	3.5	0.3
H2CA-4-F2-IGFR	RSASGSLPEQFYDFWFRQVSLSGTDK	17.6	13.8	4.1	3.4	0.3
H2CA-3-D11-IGFR	SRVTTVFHENFYDFWFRQLSDSAISG	9.3	12.8	4.2	3.0	0.3
H2CA-4-H9-IGFR	DERGGKFREDFYDFWFRQVSESFRGQ	12.2	6.9	2.3	3.0	0.3
H2CA-2-B11-IGFR	RGAVAGFHDQFYDFWFRQVSRVHKFG	8.7	5.6	1.9	3.0	0.3
H2CA-3-E8-IGFR	AICDAGFHEHFYDFWFRQVSDCGRQS	11.9	4.6	1.6	3.0	0.3
	LGYQEPFQQNFYDFWFRQVSGAENAG	13.2	6.3	2.2	2.9	0.3

# Table 10

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
H2CA-3-E6-IGFR	XXXXXXXXFHENFYDWFVRQVSXXXXXX	--	--	--	--	--
H2CA-4-F4-IGFR	WRGHGTFHEDFYDWFVRQVSGSGSST	15.7	8.7	3.1	2.8	0.4
H2CA-3-D10-IGFR	GGRVGLHENFYDWFDRQVSLRGADG	11.5	7.4	3.0	2.5	0.4
H2CA-3-E1-IGFR	CNLTAGFHEQFYHWFATQVCGDAENA	9.4	6.8	2.9	2.3	0.4
H2CA-2-B6-IGFR	ERGEDMFHENFYDWFVRQISGRQGGG	12.5	6.4	2.8	2.3	0.4
H2CA-3-E11-IGFR	TNQGVSFYDSFYGWFVRQIQYGVDSG	18.0	6.2	2.7	2.3	0.4
H2CA-4-H2-IGFR	HLADGQFHEKFYDWFVRQISSRCNDC	4.7	2.2	1.0	2.2	0.5
H2CA-3-C11-IGFR	QTFGKSLHENFYDWFVRQVSREEGGD	9.8	9.9	4.8	2.1	0.5
H2CA-2-B8-IGFR	FRTLAAQHDSFYDWFDRQVSGAAGER	9.3	3.3	1.6	2.1	0.5
	SASTHQFHENFYDWFVRQVSGAQKIL	14.6	7.9	3.9	2.0	0.5

Figure 1L (Con't)



Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFSR	IR	IGFSR/IR	IR/IGFSR
Parental	XXXXXXXXXXFYXWXXXXXXXXX	--	--	--	--	--
H2CBα-3-B12-IR	VTFTSAVFHENFYDFVRQVS	29.8	17.5	16.3	1.1	0.9
H2CBα-3-D2-IR	QSDSGTVHDRFYGWFRDT+A	26.0	1.3	20.4	0.1	16.0
H2CBα-3-D12-IR	WTDVDGFHSGFYRWQFQWER	20.6	1.7	12.1	0.1	7.0
H2CBα-3-H5-IR	VASGHVLHGQFYRWFDQFAL	24.6	2.1	14.0	0.1	6.7
H2CBα-3-B6-IR	QARVGNVHQQFYWFREVMQG	16.7	2.4	15.1	0.2	6.3
H2CBα-3-G11-IR	VGDFCVSHDCFYGWFLRESMQ	31.4	2.5	13.9	0.2	5.6
H2CBα-3-A6-IR	SGSRPVFHEQFYWFVDQLG	22.7	1.4	6.4	0.2	4.7
H2CBα-3-B1-IR	QFSAGAFHGDYGFWRALYNG	25.9	1.7	7.1	0.2	4.3
H2CBα-3-F8-IR	SRFDERLHHQFYWFPRVLNEP	33.4	6.0	25.5	0.2	4.3
H2CBα-3-E11-IR	DSVNSDLHRAFYGWFAEQWRA	23.0	4.8	19.8	0.2	4.1
H2CBα-3-G4-IR	GSVDREIHGPFYWFSEQLWG	14.0	2.2	8.5	0.3	4.0
H2CBα-3-D3-IR	SAKTPVLHDGYMWFEAQSES	24.9	2.2	6.9	0.3	3.2
H2CBα-3-C1-IR	LVVGRRFHQSFYDWFVAAAGG	23.6	2.6	8.0	0.3	3.1
H2CBα-3-C3-IR	IMWPCTFQDPFYCWFQTEQGR	27.0	5.6	16.4	0.3	2.9
H2CBα-3-G3-IR	VVGPLDIHERFYGFHQQGGA	23.3	1.1	3.1	0.4	2.8
H2CBα-3-E4-IR	VVPKAGFHEAFYWFRRQDRD	23.7	6.7	17.6	0.4	2.6
H2CBα-3-G5-IR	QSFVTSVHTRFYANFASALEM	28.8	8.3	21.9	0.4	2.6
H2CBα-3-B11-IR	SRGLGLYHSGFYGWFERQFNQ	26.7	7.0	17.2	0.4	2.5
H2CBα-3-A1-IR	GADTGAVHRRFYLWFEQLSGG	28.0	8.6	19.4	0.4	2.3
H2CBα-3-H1-IR	PGNRPTFHAEFYRWFRQAQGS	31.3	11.3	24.9	0.5	2.2
H2CBα-3-F12-IR	VAVAWGLHESFYANFENQFSD	27.2	10.6	23.9	0.4	2.2
H2CBα-3-H7-IR	GFNTGTFHDQFYFWFEAAGG	21.1	6.1	12.7	0.5	2.1
H2CBα-3-C12-IR	GDGLTAFHQGFYWFEDIQMYG	21.0	9.7	19.1	0.5	2.0
	VGVNRQFHTRFYAWFDEQLGG	26.0	12.7	24.7	0.5	1.9

Figure 1M

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXFHXFXFXWFXXXXXX	--	--	--	--	--
H2CBα-3-D11-IR	GPRGQRLHDAFYSWFDALRVN	27.8	13.0	24.8	0.5	1.9
H2CBα-3-H12-IR	LGT LAVFHEL FYGWFERQLGG	27.4	7.2	12.4	0.6	1.7
H2CBα-3-A10-IR	LGCGGFCNCFYRWFNDLADR	27.1	13.2	22.3	0.6	1.7
H2CBα-3-A5-IR	FSGWADYQSGFYQWFAEELAN	28.3	16.1	28.1	0.6	1.7
H2CBα-3-C4-IR	WGPFVSFDES FYRWFQAASDD	30.7	17.2	29.2	0.6	1.7
H2CBα-3-B8-IR	PRNEGLVHGLFYDWFORALSG	25.6	11.3	18.6	0.6	1.6
H2CBα-3-H11-IR	DEGGAPLDVMFYRWFEEAVRG	28.8	14.0	22.4	0.6	1.6
H2CBα-3-E10-IR	QSGNRGSHGAFYSWFRDVLAN	27.7	14.3	23.0	0.6	1.6
H2CBα-3-C2-IR	MRQRDGFNSFYGWFAAALGE	28.4	17.0	26.7	0.6	1.6
H2CBα-3-F6-IR	SEERKKVHSQFYSWFDRQLLG	27.3	14.5	21.8	0.7	1.5
H2CBα-3-D4-IR	PSPNAPFHGGFYDWFDWVQGS	29.0	18.9	27.1	0.7	1.4
H2CBα-3-A7-IR	FHRPGSFNTNFYQWFDQDMNQ	29.1	19.4	26.9	0.7	1.4
H2CBα-3-H4-IR	SDDSSTLNGRFYTWFMQLLD	27.2	20.1	27.9	0.7	1.4
H2CBα-3-B7-IR	QRGGGFHEGFYSWFRSQSLL	28.6	18.0	23.6	0.8	1.3
H2CBα-3-F9-IR	SGSRPVFHEQFYEWFDVQLGL	26.1	19.1	24.3	0.8	1.3
H2CBα-3-H6-IR	GGSSQAFHGAFYEWFSQQLRG	24.8	21.6	27.3	0.8	1.3
H2CBα-3-F5-IR	AFVSE RVNQRFYDWFRDQMR S	29.4	22.0	27.8	0.8	1.3
H2CBα-3-A2-IR	VRHPTRFHDEFYRWFTEQLTT	30.7	22.5	29.1	0.8	1.3
H2CBα-3-F3-IR	ARLLNIFDRGFYNWFQRQLDE	16.3	6.7	9.0	0.7	1.3
H2CBα-3-G6-IR	PSLSSNLHESFYRWFQDLVST	24.9	21.0	24.4	0.9	1.2
H2CBα-3-G7-IR	FAFGLGFHQGFYDWFAHQLEG	24.4	18.7	23.0	0.8	1.2
H2CBα-3-C5-IR	VSATVMLHREFYDWFGQLLLD	26.4	21.2	25.4	0.8	1.2
H2CBα-3-G1-IR	GGVSGVLHDRFYSWFERQLAG	26.9	21.5	26.3	0.8	1.2
H2CBα-3-E3-IR	GLGIASFHEGFYSWFTAQLGA	24.2	17.2	19.3	0.9	1.1

Figure 1M (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR IR/IGFR
H2CBα-3-A9-IR	XXXXXXFHXXFYXWFXXXXXX	30.5	21.7	24.1	0.9 1.1
H2CBα-3-C11-IR	RVDAAALNAGFYEWFRGVIQG	26.4	21.8	23.2	0.9 1.1
H2CBα-3-B4-IR	GGAGRSFHDAFYEWFRQWAG	30.9	22.0	24.3	0.9 1.1
H2CBα-3-F11-IR	EGARQGFHARFYSWFAQQLAL	24.5	22.5	23.9	0.9 1.1
H2CBα-3-G10-IR	VLLPGVVHGGFYDWFSRQLSS	28.3	23.6	27.1	0.9 1.1
H2CBα-3-D7-IR	GALSDRYNNVFDWFRQQLLG	31.4	23.6	25.3	0.9 1.1
H2CBα-3-E2-IR	PDSFMSLHQRFYSWFQAQVGT	26.8	24.0	25.7	0.9 1.1
H2CBα-3-B5-IR	RVYKANFHNEFYGWFRQQLG	28.7	25.0	26.4	0.9 1.1
H2CBα-3-C7-IR	HSGMRDVHARFYSWFSEQLSG	30.0	25.2	28.7	0.9 1.1
H2CBα-3-G9-IR	ARLLERFQDPFYEWFTLMGD	27.8	25.2	26.7	0.9 1.1
H2CBα-3-A12-IR	RNSSGNFHDKFYWNFEAQLKG	28.0	26.4	28.7	0.9 1.1
H2CBα-3-C9-IR	GSMSPVNDQFYGWFRDLVDE	32.1	28.7	31.9	0.9 1.1
H2CBα-3-B10-IR	SCTGRQFDGCFYAWFEDQLVG	33.5	30.8	33.2	0.9 1.1
H2CBα-3-E1-IR	GIAVQSLHDSFYRWFDNALGS	31.7	30.5	29.0	1.1 1.0
H2CBα-3-G12-IR	IGPPGSLHRGFYDWFAEQVEA	29.1	31.4	29.8	1.1 1.0
H2CBα-3-F7-IR	GAAGISFHRGFYDWFAAQVRD	23.2	20.7	20.3	1.0 1.0
H2CBα-3-G8-IR	GVDVTDFHKDFYSWFQRQLNG	22.8	20.9	20.4	1.0 1.0
H2CBα-3-C6-IR	WAGRAGIHGGFYEWFRNQLRG	26.7	21.2	22.0	1.0 1.0
H2CBα-3-H9-IR	LGQLAAFLHGFYEWFSFAVAA	23.4	22.5	22.0	1.0 1.0
H2CBα-3-H8-IR	VHSVSRNLNVGYQWFQDQLSG	23.5	23.4	23.2	1.0 1.0
H2CBα-3-F2-IR	LGLMAIFDRGFYGFWEQQLSG	25.5	24.3	25.2	1.0 1.0
H2CBα-3-D5-IR	VARGSSLHDDFYEWFSASQLRT	26.7	24.5	25.6	1.0 1.0
H2CBα-3-D10-IR	LGYIGALNTQFYSWFADLVGS	26.8	24.9	24.9	1.0 1.0
H2CBα-3-F10-IR	EDSRLRLHEGFYGWFRKQLGD	25.7	25.6	26.1	1.0 1.0
	GRDNMKFHS GFYDWF TQQLAG				

Figure 1M (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
H2CB $\alpha$ -3-D6-IR	XXXXXXXXHXXFYXWFXXXXX	--	--	--	--	--
H2CB $\alpha$ -3-H3-IR	AGVMGGFHQEFYLWFERALSN	27.9	26.0	25.8	1.0	1.0
H2CB $\alpha$ -3-F4-IR	AGHVGVYDGYGWFREQLGA	27.0	26.9	26.2	1.0	1.0
H2CB $\alpha$ -3-E9-IR	FVQ $\overline{N}$ IGFDYDFYGFVREVEK	31.2	27.2	27.7	1.0	1.0
H2CB $\alpha$ -3-H10-IR	PVGIGGLHRAFYQWFQSQVDA	31.6	27.7	28.2	1.0	1.0
H2CB $\alpha$ -3-G2-IR	GS $\overline{RQ}$ EADHQAFYDWFNLVLGV	26.9	27.9	28.8	1.0	1.0
H2CB $\alpha$ -3-B2-IR	AGGRKPFHDDFYGWF $\overline{RDL}$ AE	29.1	28.1	28.8	1.0	1.0
H2CB $\alpha$ -3-E8-IR	DLASHGFHDAFYNWF $\overline{SVQ}$ LNS	29.4	28.1	28.2	1.0	1.0
H2CB $\alpha$ -3-E5-IR	GSNGGVHGVQFYAFV $\overline{FAL}$ SG	31.5	28.4	29.1	1.0	1.0
H2CB $\alpha$ -3-E6-IR	RGRASTFHDGYGWF $\overline{SQQL}$ RF	33.0	28.7	28.9	1.0	1.0
H2CB $\alpha$ -3-E7-IR	SPARRVSHHDFYGF $\overline{WFAKQ}$ LES	29.6	29.0	28.1	1.0	1.0
H2CB $\alpha$ -3-C8-IR	SSDVGA $\overline{FHS}$ AFYDWF $\overline{KAQ}$ LSG	30.4	30.2	30.2	1.0	1.0
H2CB $\alpha$ -3-A4-IR	PTVHRAFD $\overline{DLF}$ YGWF $\overline{AKQ}$ VED	31.9	31.2	31.5	1.0	1.0
H2CB $\alpha$ -3-D1-IR	SSNTVGLDERFYAF $\overline{VDQ}$ LGA	32.2	31.9	32.6	1.0	1.0
H2CB $\alpha$ -3-B9-IR	PGAAEGF $\overline{HS}$ AFYDWF $\overline{AQAV}$ SG	32.9	32.5	31.5	1.0	1.0
H2CB $\alpha$ -3-D8-IR	MRSEASFHVEFY $\overline{SWFEQ}$ LRS	33.2	33.8	33.3	1.0	1.0
H2CB $\alpha$ -3-F1-IR	VSRYG $\overline{GQD}$ GFYHWF $\overline{SDLLK}$ G	26.3	20.2	19.1	1.1	0.9
H2CB $\alpha$ -3-A11-IR	RPSSGGLHYGFYHWF $\overline{RVQ}$ EEM	28.8	28.0	26.4	1.1	0.9
H2CB $\alpha$ -3-A3-IR	SNIEEHFM $\overline{Q}$ FYRW $\overline{FSDAL}$ GN	20.5	21.5	17.7	1.2	0.8
	ANDCLGLHAGFYGWF $\overline{ACQL}$ GG	30.4	29.6	21.8	1.4	0.7

Figure 1M (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
H2CB $\beta$ -3-E8-IR	XXXXXXXXFHXFXFXWFXFXFXFXFXFX	15.9	1.9	11.8	0.2	6.1
H2CB $\beta$ -4-F8-IR	TGHRGLGLDEQFYWFWFRDALSG	13.4	0.8	2.6	0.3	3.4
H2CB $\beta$ -3-C4-IR	VLTSNTLHQRFYSWFAAARRE	21.1	1.3	4.0	0.3	3.1
H2CB $\beta$ -3-D5-IR	CVAQGGFQSSFYCWFAGLDID	14.0	3.3	10.2	0.3	3.1
H2CB $\beta$ -3-E6-IR	NGQSSRFHTAFYDWFAAQLSG	5.7	0.7	2.1	0.3	3.1
H2CB $\beta$ -4-G12-IR	SVPRGTVHDAFYQWFREVALG	6.8	1.8	5.4	0.3	3.1
H2CB $\beta$ -4-F4-IR	GARGSTFHDQFYEWFWVQLGD	17.9	1.9	5.6	0.3	3.0
H2CB $\beta$ -4-F11-IR	PPGMNGFHTSFYSWFDQLGD	15.0	1.7	4.8	0.3	2.9
H2CB $\beta$ -3-E5-IR	AVGTLGYHSGFYRWFERQLGG	17.0	1.8	5.0	0.4	2.8
H2CB $\beta$ -4-F2-IR	ELQARGVHRNFYRWFEAQVSG	15.9	1.3	3.4	0.4	2.6
H2CB $\beta$ -4-G4-IR	HRVARAFHEQFYDWFEKAVSG	8.7	1.4	3.5	0.4	2.6
H2CB $\beta$ -3-C8-IR	GAMEPDYHRSFYQWFFAALGE	4.9	1.4	3.2	0.4	2.3
H2CB $\beta$ -4-F10-IR	CPDRQSVDDRFYNWFADALAS	10.2	1.0	2.4	0.4	2.3
H2CB $\beta$ -4-H4-IR	GGAQISFHERFYQWFLQEAAG	20.8	4.2	9.5	0.4	2.3
H2CB $\beta$ -4-G6-IR	HKRGIVQHGAFYAWFDSLSSG	14.5	5.6	8.5	0.7	1.5
H2CB $\beta$ -4-H1-IR	QASDNRS <del>GDG</del> QFYLWFEKLLSS	17.0	10.1	13.2	0.8	1.3
	DRGRMGVDEGFYNWFARQMQE					

Figure 1M (Con't)

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Design	XXXXXXXXFHXXFYXWFXXXXXX	--	--	--	--	--
Parental	VTFTSAVFHENFYDWFVRQVS	29.8	17.5	16.3	1.1	0.9
H2CB-3-D2-IGFR	TASQECFDDGFYGWFAWRCT	22.9	18.6	11.8	1.6	0.6
H2CB-3-C12-IGFR	SLDWRWSEEPFYRWFQALAG	17.3	19.6	13.0	1.5	0.7
H2CB-3-B11-IGFR	CMSLSDCHRKIFYGWFKSQGGE	24.6	17.1	11.9	1.4	0.7
H2CB-4-E2-IGFR	LALCRRSPGSFYGWFAQAVGC	22.4	21.0	16.5	1.3	0.8
H2CB-3-A5-IGFR	PRSATMSDGGFYWWFASQLGL	28.8	26.1	22.6	1.2	0.9
H2CB-4-G12-IGFR	LRRSSVFHDPPYE*ISRLVGG	23.7	23.8	19.4	1.2	0.8
H2CB-3-B2-IGFR	ARLQQQFHGGFYEWFRQVSP	23.0	19.9	16.4	1.2	0.8
H2CB-3-D1-IGFR	AQLDNLCHPEPFYSWFCVATRE	21.5	19.5	15.7	1.2	0.8
H2CB-3-B6-IGFR	WTCDTAFHQDFYQWFCDKLGV	16.3	4.5	3.7	1.2	0.8
H2CB-4-F7-IGFR	GKEGFGLDLDRDFYWWFREQLGP	22.0	19.0	18.0	1.1	0.9
H2CB-4-G8-IGFR	GRAPSSFDGDFYCWFRNQVQS	20.2	18.6	16.5	1.1	0.9
H2CB-3-D4-IGFR	DVEAETQHRLFYAWFLSQLGS	21.9	18.3	16.9	1.1	0.9
H2CB-3-D5-IGFR	ISVTAVFHGDFYGWFNEQVSK	21.4	17.9	16.4	1.1	0.9
H2CB-4-E6-IGFR	NSEHGRLDVDFYGWFAFARVIQQ	19.6	15.8	14.8	1.1	0.9
H2CB-3-C2-IGFR	GPLGDGCQDGFYGMFCQVST	18.8	12.2	10.8	1.1	0.9
H2CB-3-A6-IGFR	KRSAYNFHDPPFYDWMFRMQLSG	26.8	29.0	28.1	1.0	1.0
H2CB-4-H12-IGFR	ASEPGGYLDPPFYGWFREQLRA	23.9	28.3	28.1	1.0	1.0
H2CB-3-B10-IGFR	NRGDGGVHSGGFYNWFRQLLSG	27.1	27.5	27.3	1.0	1.0
H2CB-4-F11-IGFR	ASKGSSLHNDFYGWFAQQLAR	25.5	25.5	24.6	1.0	1.0
H2CB-4-G11-IGFR	ANVSMWIQVGFDWFDQAQLRQ	25.3	25.4	25.3	1.0	1.0
H2CB-4-E12-IGFR	RTSPGSLHDPFYDWFQQQLGG	27.8	24.9	24.7	1.0	1.0
H2CB-4-G10-IGFR	PGVMSSFHGGFYSWFREQLNG	25.1	24.6	24.2	1.0	1.0
H2CB-3-B9-IGFR	CLANSEDHDSFYGWFCQALGG	25.6	23.3	23.7	1.0	1.0
H2CB-3-B7-IGFR	GGSMGGMHGSFYEWFAQLRS	24.0	23.2	23.5	1.0	1.0
H2CB-4-H4-IGFR	RPQGGSIHAGFYQWFRDVAAG	23.5	23.1	23.8	1.0	1.0

**Figure 1N**

Clone	D sign	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
H2CB-4-H10-IGFR		XXXXXXFHXXFYXWFXXXXXX	--	--	--	--	--
H2CB-4-H5-IGFR		GALSSLFDAAFYDWFNRQLG	21.9	22.4	23.3	1.0	1.0
H2CB-4-G7-IGFR		KVDLRGFHDGFYGFARQLAG	22.3	22.3	21.6	1.0	1.0
H2CB-4-F4-IGFR		CSGLQRCHDSFYSWFESVRE	23.1	21.6	20.6	1.0	1.0
H2CB-3-D8-IGFR		DSLGISFHEGFYDWFRRQLDM	21.3	20.9	21.3	1.0	1.0
H2CB-4-E4-IGFR		SGVFNGTFYDWFRIQLGE	20.0	20.5	21.6	1.0	1.0
H2CB-4-E5-IGFR		GYREMRSDLGFYQWFRDQLGL	21.6	20.5	21.2	1.0	1.0
H2CB-4-E8-IGFR		SVFMQHHDHVGFYAWFRSLMEE	22.0	19.9	20.9	1.0	1.0
H2CB-3-D12-IGFR		FRHITVDRSFYGFVFEQLRG	21.1	19.7	20.7	1.0	1.1
H2CB-4-G9-IGFR		WAGGSDVDGSFYDWFQRLLAS	26.6	17.3	16.8	1.0	1.0
H2CB-3-C8-IGFR		GLQNVSFHSGFYENFARQVSQ	21.6	14.5	15.2	1.0	1.1
H2CB-3-A12-IGFR		SRVSDPYHVGFYQWFEVVRG	20.8	13.4	13.9	1.0	1.0
H2CB-3-B12-IGFR		MGGATFFHTGFYDWFAAQLQH	28.6	27.5	29.2	0.9	1.1
H2CB-3-A9-IGFR		RPASRPFHSGFYQWFAQLSH	27.8	25.2	27.1	0.9	1.1
H2CB-3-A3-IGFR		GLAPGNFHEDFYRWFOEQLTG	27.7	24.3	25.7	0.9	1.1
H2CB-3-B4-IGFR		TAAISDFNSLFYGWFEQLSS	26.9	24.1	26.5	0.9	1.1
H2CB-4-E7-IGFR		LDEDLPQHAGFYGWFAEALGV	25.8	23.8	25.3	0.9	1.1
H2CB-4-G6-IGFR		ASHKSAFDDNFYRWFSWQLRD	24.6	21.6	24.0	0.9	1.1
H2CB-4-E9-IGFR		HTGAGDLHGAFYNNWFLEQLGG	22.4	21.1	23.0	0.9	1.1
H2CB-4-H2-IGFR		RRGRDGFHGGFYDWFAAQLSD	24.3	20.7	22.0	0.9	1.1
H2CB-3-A10-IGFR		GNFREAFHADFYSWFERQLQS	21.6	20.2	21.9	0.9	1.1
H2CB-3-C4-IGFR		RDTLPAFHQHFYQWFEKQVSA	24.3	19.9	21.5	0.9	1.1
H2CB-3-B5-IGFR		ERETAAFGQAFYQWFRDQIAG	23.1	19.2	22.0	0.9	1.1
H2CB-4-G4-IGFR		WGEKGGFYDWFYDQLGWEP SH	24.2	18.8	20.7	0.9	1.1
H2CB-3-D9-IGFR		SLVAADLHEGFYGWFRS QLGG	21.7	18.7	21.2	0.9	1.1
H2CB-3-C3-IGFR		TSEVGDFHAEFYSWFEIQLGR	24.4	18.6	20.0	0.9	1.1
H2CB-3-D3-IGFR		TGADGLLHARFYAWFEEQLRE	20.3	18.4	21.1	0.9	1.1
H2CB-4-F2-IGFR		RRSDSSLHRSFYDWFVSQLLN	22.5	18.3	21.3	0.9	1.2
		SESKYLLHSGFYGWFEAQLRG	18.0	16.8	18.3	0.9	1.1

Figure 1N (Con't)

Clone	Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		XXXXXXXXFHXFXFXWXXXXXXXX	--	--	--	--	--
H2CB-4-H1-IGFR		HGVIRADHTGFYGFWSKQLSD	18.3	15.3	16.5	0.9	1.1
H2CB-4-F9-IGFR		LINA.VFRRGFYAWFEEQVSK	22.9	14.4	15.3	0.9	1.1
H2CB-4-E10-IGFR		LQRYIGFHDPPYDWFSLSG	26.1	20.1	24.5	0.8	1.2
H2CB-4-F8-IGFR		MRTAELFHVGFYDWFDAQLMD	21.5	14.8	19.0	0.8	1.3
H2CB-3-A8-IGFR		WAPPDALHGQFYRWFORQLDQ	20.7	14.7	18.2	0.8	1.2
H2CB-4-F1-IGFR		AVHAATFHDDFYRWFEQVGS	22.2	14.6	18.8	0.8	1.3
H2CB-3-C6-IGFR		FDAVHGFDGGFYGFWKRELQR	15.7	7.8	10.2	0.8	1.3
H2CB-4-E11-IGFR		QAGGMEFHGAFYNWFLQQLSG	26.1	17.6	24.1	0.7	1.4
H2CB-3-D6-IGFR		GRSVSRMNAEFYQWFGHQLAA	21.6	13.0	18.8	0.7	1.5
H2CB-4-F3-IGFR		AAVNSLFHDEFYLFWFQDQLDG	17.3	11.1	16.4	0.7	1.5
H2CB-3-A4-IGFR		QLGMDWFHADFYEWFLAQLPS	27.4	11.0	14.8	0.7	1.3
H2CB-3-B1-IGFR		RLAGSGIHEGFYGFWFDQLLA	20.0	11.0	15.2	0.7	1.4
H2CB-3-C5-IGFR		GREIGGVHDGFYDWFRRQSEQ	19.9	10.5	15.6	0.7	1.5
H2CB-4-F6-IGFR		VRSEQRFDSSFYQWFNDLLMS	18.6	10.1	14.6	0.7	1.4
H2CB-3-B8-IGFR		QSPYGFHDFYRWFLQQTGM	20.7	6.9	9.5	0.7	1.4
H2CB-3-C7-IGFR		FQCGAAFHVDYRWFTCQEQF	16.2	1.8	2.5	0.7	1.4
H2CB-4-H7-IGFR		GAFGSEFHEQFYRWFEALSF	21.8	14.1	22.7	0.6	1.6
H2CB-4-F5-IGFR		EHTSYQIHRQFYEWFDRLGR	12.9	4.0	7.2	0.6	1.8
H2CB-4-G1-IGFR		SGTAADLHSRFYGFWFALQARE	20.4	10.3	19.7	0.5	1.9
H2CB-3-D11-IGFR		EGFGVLFHGQFYRWFLQLDG	24.1	8.8	18.6	0.5	2.1
H2CB-3-D7-IGFR		QQSAGHPHSSFYLFWSELGA	22.1	6.5	13.6	0.5	2.1
H2CB-3-C10-IGFR		YLQRAGFHRSFYGFWDQALRD	21.7	5.1	10.4	0.5	2.0
H2CB-4-E3-IGFR		MWLWATLHSDFYSWFEQVVS	20.3	4.6	8.9	0.5	1.9
H2CB-3-C1-IGFR		GANALGFKDRFYEWFAAQLWD	22.3	6.7	15.7	0.4	2.3
H2CB-4-G2-IGFR		GSGLYVFHWGFYDWFEEQMG	19.9	3.3	10.7	0.3	3.3
H2CB-3-A11-IGFR		LDKGWGFDDLQFYRWFEAATRA	23.9	2.5	7.7	0.3	3.1
H2CB-4-G5-IGFR		QRSAREFHADFYDWFLLRLTP	19.3	2.5	7.9	0.3	3.1
H2CB-4-F12-IGFR		DQRMGSFHGEFYRWFEETLLS	16.7	1.7	5.4	0.3	3.1

Figure 1N (Con't)



Clone	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
Design	$X_n - FyxWF - X_m$	--	--	--	--	--	
20E2A-3-B11-IR	GRFYGFQDAIDQLMPWGFD <sup>P</sup>	24.6	1.4	23.6	0.1	16.8	
20E2Bβ-3-E3-IR	IQGWEPFYGFDDVVAQMFE <sup>E</sup>	23.0	0.9	15.3	0.1	16.3	
rB6-3-F6-IR	RYGRWG <sup>L</sup> AQQFYDWFDR	40.9	1.0	13.3	0.1	13.3	
rB6-4-F9-IR	RRLGSLSTQFYNWFAE	34.1	1.0	12.6	0.1	12.6	
20E2Bα-3-A8-IR	ASAYTPFYQW <sup>F</sup> ADVVSEYMQQ	35.4	7.4	34.4	0.2	4.6	
A6L-4-F6-IR	PYRMET <sup>E</sup> KNFYDWFVAQLQ	28.9	4.1	18.1	0.2	4.4	
20E2Bα-4-H9-IR	SAVHFQFYKWF <sup>D</sup> NLLPVPLSA	37.8	9.4	26.7	0.4	2.9	
20E2Bα-3-B1-IR	VPVNKSFYRW <sup>F</sup> QLVLGGSDDW	41.8	12.9	36.8	0.4	2.9	
20E2Bβ-4-F9-IR	QSPRASFYGW <sup>F</sup> DDVLR <sup>A</sup> AGW	25.9	4.2	10.1	0.4	2.4	
20E2Bβ-3-E9-IR	TGFYEW <sup>F</sup> YEQLHSRMLPNPLD	27.0	7.7	17.2	0.5	2.2	
20E2Bβ-3-E10-IR	RRGVGGFYGF <sup>S</sup> QQLOGMGVA	22.2	2.6	5.5	0.5	2.1	
20E2Bα-3-C12-IR	SSQDRRFYRW <sup>F</sup> EQAIVGGRDG	39.0	6.7	12.0	0.6	1.8	
20E2Bβ-3-C12-IR	TRGQLGFYNW <sup>F</sup> QALSTSGMG	20.2	2.2	3.8	0.6	1.8	
20E2Bβ-3-E7-IR	CADLNAFYQW <sup>F</sup> CGVLD <sup>R</sup> GS <sup>D</sup> H	9.2	1.2	1.9	0.6	1.6	
20E2Bβ-3-E11-IR	TLIQDQFYWW <sup>F</sup> SDLLSAEPGD	20.7	1.3	2.1	0.6	1.6	
20E2Bα-3-B11-IR	IDQLDAFYRW <sup>F</sup> DGVMLGMGDP	36.0	20.7	32.8	0.6	1.6	
NNKH-4-G2-IR	RGGTTFYEW <sup>F</sup> ESALRKHGAG	10.8	6.3	8.9	0.7	1.4	
20E2Bα-3-A7-IR	RGLDQD <sup>F</sup> YRW <sup>F</sup> QNLVGEYDR	19.0	4.2	5.5	0.8	1.3	
20E2Bα-4-G12-IR	MQGHRGFYGF <sup>W</sup> FARVLEQDRGW	37.0	22.3	29.5	0.8	1.3	
20E2Bα-3-C11-IR	ERLHLRFYEW <sup>F</sup> DTVIGQGS <sup>D</sup>	37.3	26.8	34.8	0.8	1.3	
20E2Bα-3-C10-IR	MHVQSDFYHWF <sup>Q</sup> SLLGQGGPD	37.7	24.8	30.5	0.8	1.2	

## Figure 10

Clone Design	Sequence $X_n - Fy \times WF - X_m$	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2B $\alpha$ -3-D7-IR	TMGTQGFYRWFNVVKEHLSG	35.4	26.9	31.3	0.9	1.2
20E2B $\alpha$ -3-A12-IR	ITHNRGFYSWFLDVVQGGAGA	31.7	22.0	23.3	0.9	1.1
20E2B $\alpha$ -3-D10-IR	VRRDAGFYQWFADILTQDFE	32.7	27.3	29.1	0.9	1.1
20E2B $\alpha$ -4-G7-IR	MQLQDEFYNWFRGIMLNDGQD	34.2	29.0	30.7	0.9	1.1
20E2B $\alpha$ -4-F5-IR	GIRSSGFYQWFDRLAGVGDG	33.8	32.1	34.0	0.9	1.1
20E2B $\alpha$ -3-C9-IR	ANLNSQFYSWFASVTGEASPS	39.4	33.2	35.5	0.9	1.1
20E2B $\alpha$ -3-A4-IR	QSPRASFYGWFDLVLRAAGVV	38.2	31.6	35.9	0.9	1.1
20E2B $\alpha$ -4-E12-IR	MQRNQGFSWFDDLVSTGV	36.0	30.8	29.7	1.0	1.0
20E2B $\alpha$ -4-E11-IR	ASGDFPFYAWFLEQLRVANGS	35.1	31.2	30.7	1.0	1.0
20E2B $\alpha$ -4-E8-IR	SGTPYGFYRWFSALASATSG	36.1	30.5	30.7	1.0	1.0
20E2B $\alpha$ -4-H10-IR	QGVGEGFYEWFDAMGDVRPW	38.9	30.6	30.7	1.0	1.0
20E2B $\alpha$ -4-F6-IR	DNMSGGFYRWFAQVVDSSGD	34.9	33.2	32.0	1.0	1.0
20E2B $\alpha$ -4-G4-IR	RGTDDTFYGFWDQLLQWCDD	34.1	33.7	32.2	1.0	1.0
20E2B $\alpha$ -4-F8-IR	TVDHTQFYDWFSRVLGESGSA	37.7	32.0	32.7	1.0	1.0
20E2B $\alpha$ -4-G5-IR	GRQDREFYWFELQAGGMDGD	34.9	33.9	33.4	1.0	1.0
20E2B $\alpha$ -3-B10-IR	RLLLGGFYEWFDQVLKETKEV	38.2	34.9	33.6	1.0	1.0
20E2B $\alpha$ -3-C7-IR	GVLSTGFYEWFAQLHGLAAG	37.6	34.2	34.8	1.0	1.0
20E2B $\alpha$ -3-C5-IR	PAVGQSFYGWFEAVLRGSKAG	40.4	36.0	35.6	1.0	1.0
20E2B $\alpha$ -3-B9-IR	SNGISGFYEWFAAQVQTSDFQ	39.6	35.8	37.1	1.0	1.0
A6L-4-F11-IR	LLGLSQAAAYANFYDWFVSQLA	33.1	4.6	4.6	1.0	1.0
20E2B $\alpha$ -3-C2-IR	VPNSWMFYNWFAEQIEGSEGE	44.1	40.0	38.1	1.0	1.0
20E2B $\alpha$ -3-B2-IR	ARRADGFYDWFREQVSGSAVQ	43.1	40.1	39.0	1.0	1.0
20E2B $\alpha$ -4-G2-IR	GVVEGTFFYEWFDRLLGVCQGD	34.1	33.6	29.8	1.1	0.9
20E2B $\alpha$ -4-H6-IR	SHLTDPFYQWFDQLRAGVRG	39.4	36.0	31.9	1.1	0.9

Figure 10 (Con't)





Clone	Design
R40-3	B6-IGFR
R40-X	E5-IGFR
R40-X	B5-IGFR
R40-4	9-IGFR
R40-3	G6-IGFR
R40-4	12-IGFR
R40-3	A5-IGFR
R40-X	C6-IGFR

**Sequence**

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX  
AETPAQVGNRLWSVPGEHWNTPDPFYHKLSELLRESGA  
RHLTNAELGVQSPEVLSRLFDPGDIPYRALSHLVRGMGPP  
RGGMDRQWLVDGARHRLERRSVQDNTDDFYGLRLILVDGF  
GPPDSFDVTTEKGDMAI LNVRFPDPSHSLDFNDQTIFYFLDL  
GGTYFRGQVAQSNESLLRVNLFQLLEALAAASPRT  
APF DARLSAPRFQWSPRTWXQSLSYGEGWSCGSFYDCLSII  
MGSSQFQDTRPSSQQAYSHSLSDSGWGTA NWIFLRALEG L  
SGAAHEGNOGRERSTH LAANIN DHPGDAGI WLGYSWLS

[illegible]

—

**FIGURE 2C**



Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20C-3-G3-IGFR	TFYSCLASLLTGTPQPNRGPWERC	33.1	32.3	1.2	27.0	<0.1
20C-4-C7-IGFR	FFYDCLAALLQGVARYHDLCAVEIT	35.3	28.0	1.3	21.8	<0.1
20C-3-F6-IGFR	DRDFCRFYERLTALVGGQVDGGWPC	33.5	26.1	1.9	14.1	0.1
20C-3-A1-IGFR	SSYGCDGFYLMFLSLGLVASQLEEC	26.5	20.8	1.5	13.7	0.1
20C-3-A4-IGFR	QFYGCLLDLSLGVPSFGWRRRCITA	17.7	8.8	1.2	7.6	0.1
20C-3-E4-IGFR	FFYRCLSRLLGGQLGSLGLSCIGD	37.7	7.7	1.3	6.0	0.2
20C-4-D11-IGFR	DLFYCMMQLATAGVGSGLGVPVCG	33.3	17.2	6.1	2.8	0.4
20C-4-F7-IGFR	CDFYCALSRLSGQPRDRMPNYPGTS	31.2	28.9	17.0	1.7	0.6
20C-3-B2-IGFR	GSACDGFYACLHALVQGPGEW	37.7	35.2	30.9	1.1	0.9

FIGURE 2E





Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6L-4-G6-IGFR	AETPAQVGWNRRLMSVWPGEHWNTVDPFYHKLSELLRESGA	--	--	--	--	--
B6L-4-G10-IGFR	AETPAQVGGRDLMSVWPGEHWNTVDPFYHKLSELLRESGA	7.3	22.1	--	--	--
B6L-4-G3-IGFR	AE?PAQVGWNRRLMSVWPGE?WNTVDPFYHKLSELL?ESGA	5.5	21.8	--	--	--
B6L-3-F10-IGFR	AETPAQVGWNRRLMSVWPGEHWNTVDPFYHKLSELLRESGA	5.8	18.1	--	--	--
B6L-4-D2-IGFR	AETPAQVGWNRRLMSVWPGEHWNTVDPFYHKLSELLRESGA	6.7	17.4	--	--	--
B6L-3-H10-IGFR	AETPAQVGWNRRLMSVWPGEHWNTVDPFYHKLSELLRESGA	6.5	15.9	--	--	--
B6L-4-B12-IGFR	DETSAQVGWNRRLMSDWPGEQWNTLDPFYHKLSELLRESGA	5.9	15.2	--	--	--
B6L-3-A9-IGFR	GETPAQVGWNRRLMSVWPAEHWSTVDPFYHKLSELLRESGA	6.3	14.8	--	--	--
B6L-4-C4-IGFR	AETAAQVGWNRRLQSVWPGEHWNSVDPFYHKLSELLRESGA	5.2	14.8	--	--	--
B6L-4-E3-IGFR	AEAPDQVGQNRRLMSVWPGEHWNTVDPFYHKLSELLRESGA	5.4	11.9	--	--	--
B6L-4-A12-IGFR	PETPAQVGWNRRLQSGWPGGEHWNTVDPFYHKLSELLRESGA	4.4	11.1	--	--	--
B6L-4-D5-IGFR	AQTPAQVGWNYRLSSVWPGEHWNTVDPFYHKLSELLRESGA	3.0	10.4	--	--	--
B6L-3-A10-IGFR	AETPAQVGWNRRLMSVWPGEHWNTVDPFYHKLSELLRQSDA	4.7	10.3	--	--	--
B6L-3-B9-IGFR	AETPAQVGWNRRLMSVWPGEH*NTVDPFYHKLSELLRESGA	10.9	9.7	--	--	--
B6L-3-H9-IGFR	AETPAQVGWNSLQSVWPGEHWNT?DPFYHKLSELLRESGA	2.9	9.1	--	--	--
B6L-4-A5-IGFR	AESPAQVGSNRLQSVWSGEHWNTVDPFYHKLSELLRESGA	4.5	8.8	--	--	--
B6L-3-G10-IGFR	AETPAQVGQYRLSSVWPGEHNGNTVDPFYHKLSELLRESGA	2.4	8.0	--	--	--
B6L-4-D4-IGFR	DETPAHVGWNRPPQSAWPGGERWNTVDPFYHKLSELLRESGA	4.2	7.5	--	--	--
B6L-4-F11-IGFR	AGTPAQVGWNRRLRSVQPDDEHWNTVDPFYHKLSELLRESGA	2.5	7.4	--	--	--
B6L-4-F12-IGFR	AETPAQVGWNRRLQSVWPGEHWNP?DPFYHKLSELLRESGA	2.4	6.8	--	--	--
B6L-4-E12-IGFR	AETPAQVGWNRRLQSVWPGEHWNTVDPFYHKLSELLRESGA	2.1	6.4	--	--	--
B6L-4-E10-IGFR	AETPAQVGWNRRLMSVQPGGEHWNTVDPFYHKLSELLRESGA	2.7	5.9	--	--	--
B6L-3-G9-IGFR	AETPAQVGWNRRLMSVWPGEHWNTVDPFYHKLSELLRESGA	1.9	3.9	--	--	--
		1.8	3.6	--	--	--
		1.2	2.5	--	--	--

FIGURE 2G

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFsR/IR	IR/IGFsR
B6H $\alpha$ -3-F5-IR	OOUUUUUUJJJDPFYHKLSELXXOO	42.7	9.6	17.9	0.5	1.9
B6H $\alpha$ -2-D10-IR	GGAVAAAVVGSRADPFYHKLSELVQGS	20.8	1.7	1.1	1.5	0.6
B6H $\alpha$ -3-F1-IR	SGGGQQRKAIATSDDPFYHKLSELLGG	22.5	2.4	1.3	1.8	0.5
B6H $\alpha$ -3-E6-IR	CSMAAAEAGDDDDPFYHKLSELCOGS	18.2	2.3	1.2	1.9	0.5
B6H $\alpha$ -1-B8-IR	CGAKMTGTPNDPFYHKLSELLQRG	44.6	5.2	2.1	2.5	0.4
B6H $\alpha$ -2-D5-IR	CCVEAAEAVGRRGDPFYHKLSELTGCC	39.6	2.3	0.9	2.6	0.4
B6H $\alpha$ -1-B3-IR	SRVVTMVIKRGSPDPFYHKLSELVQGR	33.1	3.2	1.1	2.9	0.3
B6H $\alpha$ -3-E5-IR	GCITAENGAGDPFYHKLSELGGCS	28.8	2.9	1.0	2.9	0.3
B6H $\alpha$ -4-H9-IR	RCGDEEGWQENRRDDPFYHKLSELFGGC	17.4	6.4	2.1	3.0	0.3
B6H $\alpha$ -2-D8-IR	GCEVIAAEGRRDDPFYHKLSELCOGG	19.3	3.0	1.0	3.0	0.3
B6H $\alpha$ -3-E4-IR	SSETAKMVTGTRDDPFYHKLSELVQGS	43.1	8.7	2.8	3.1	0.3
B6H $\alpha$ -3-F7-IR	WLCDGGWKQRRPPGDPFYHKLSELIDCG	41.5	3.1	1.0	3.1	0.3
B6H $\alpha$ -1-A3-IR	SRVAATKEKRPSDDPFYHKLSELLQGS	37.4	2.6	0.8	3.3	0.3
B6H $\alpha$ -4-H10-IR	SRAKVEAEMPDSGDPFYHKLSELLASG	50.5	29.5	8.6	3.4	0.3
B6H $\alpha$ -3-F6-IR	GGAAKTIVVVGSPDDPFYHKLSELLQGS	48.9	19.7	5.7	3.5	0.3
B6H $\alpha$ -3-F3-IR	CGVGEQMEVTDGDDPFYHKLSELLWSC	18.1	15.6	4.3	3.6	0.3
B6H $\alpha$ -4-G8-IR	SGETATIEGPSNDPFYHKLSELIWGS	32.3	6.1	1.7	3.6	0.3
B6H $\alpha$ -2-D1-IR	GGTKAVAKVGTDRDDPFYHKLSELLQGS	11.7	5.4	1.3	4.2	0.2
B6H $\alpha$ -3-E7-IR	GCEVIVEEGDSADPFYHKLSELCOGS	47.0	5.6	1.3	4.3	0.2
B6H $\alpha$ -2-D6-IR	GCAVVEEAERSRGDPFYHKLSELIQGC	33.5	4.4	1.0	4.4	0.2
B6H $\alpha$ -3-F10-IR	GRTMAVMAAGGDDPFYHKLSELVQGG	47.2	8.8	1.9	4.6	0.2
B6H $\alpha$ -3-E8-IR	GCVVEWQKWHGASDPFYHKLSELGGCS	47.6	5.3	1.1	4.8	0.2
B6H $\alpha$ -2-C10-IR	RGKTAAVIVGRPADPFYHKLSELLQGG	46.9	5.8	1.1	5.3	0.2
B6H $\alpha$ -2-C7-IR	SGAKVIVVTGSDGDPFYHKLSELLQGS	45.1	6.7	1.0	6.7	0.1
	RGIVAMVEATEVGSDDHDPFYHKLSELVQGS					

FIGURE 2H

**FIGURE 2H (Con't)**

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6Hβ-3-D7-IR	OOUUUUUUJJDDPFYHKLSELXXOO	--	--	--	--	--
B6Hβ-3-B2-IR	RGVEMKAIWGTNPDPFYHKLSELSSGS	39.5	27.1	26.3	1.0	1.0
B6Hβ-3-G5-IR	CSAVKMAEAGDPSDPFYHKLSELCOGS	34.3	34.4	35.4	1.0	1.0
B6Hβ-3-H1-IR	RGGDGDPFYHKLSELMOSS	35.3	35.0	35.6	1.0	1.0
B6Hβ-3-A5-IR	WLCKRQTHDPDPFYHKLSELACGR	36.8	35.4	36.5	1.0	1.0
B6Hβ-3-H11-IR	SSKVVKATVGTGPHDPFYHKLSELQGS	34.9	35.5	35.9	1.0	1.0
B6Hβ-3-C2-IR	GCAAIAVATGNDNDPFYHKLSELQOGR	37.7	36.4	37.6	1.0	1.0
B6Hβ-3-C8-IR	GCAAVVKETHDPDPFYHKLSELHGC	37.4	36.5	37.2	1.0	1.0
B6Hβ-3-A11-IR	SCAAEKEVAGTARDPFYHKLSELMQSS	37.0	37.7	39.5	1.0	1.0
B6Hβ-3-B7-IR	CSVAVGDSGDPFYHKLSELQOGR	40.4	38.2	39.1	1.0	1.0
B6Hβ-3-B4-IR	WQRNKQIIIGTPDDPFYHKLSELLEGS	35.4	38.3	39.5	1.0	1.0
B6Hβ-3-E12-IR	RSAAAKAVIGSPNDPFYHKLSELIQGG	37.8	39.0	39.4	1.0	1.0
B6Hβ-3-A4-IR	WLCDRDGRDEQPDWPFYHKLSELVSCGR	33.5	39.4	41.3	1.0	1.0
B6Hβ-3-B8-IR	GSVAAAKKTGSSDDPFYHKLSELQOGR	39.0	39.8	41.1	1.0	1.0
B6Hβ-3-C5-IR	GCAVTTMTMRSPADPFYHKLSELQOGR	40.1	40.4	41.1	1.0	1.0
B6Hβ-3-A2-IR	GCKVDDE*ARSSDPFYHKLSELKQGR	35.8	40.7	40.7	1.0	1.0
B6Hβ-3-B5-IR	GCKAVVEVKDHGDDPFYHKLSELQOGR	40.8	40.7	39.5	1.0	1.0
B6Hβ-3-C12-IR	CSTVTVSGSDDPFYHKLSELQOGR	40.7	40.9	42.6	1.0	1.0
B6Hβ-3-B11-IR	RSVTAKVEVGSDDPFYHKLSELQOGR	41.1	41.4	41.9	1.0	1.0
B6Hβ-3-C3-IR	GSRRQKIEVGTNPDPFYHKLSELQOGR	40.0	41.9	41.6	1.0	1.0
B6Hβ-3-B5-IR	LCDEKQRTVTGTNDPFYHKLSELQOGR	39.8	42.0	41.3	1.0	1.0
B6Hβ-3-C4-IR	SCMVEGPNDDPFYHKLSELQOGR	40.7	42.6	43.3	1.0	1.0
B6Hβ-3-G7-IR	GGAUVVAMGNDPDPFYHKLSELQOGR	43.0	42.7	44.0	1.0	1.0
B6Hβ-3-C11-IR	GGVIKAMKAGPDDPFYHKLSELQOGR	42.7	43.9	45.4	1.0	1.0
	GCIIAEKVVGPDDPFYHKLSELQOGR	41.1	42.3	36.6	1.2	0.9
	GCEKVVAVAGNAGDPFYHKLSELQOGR	4.1	2.4	2.1	1.1	0.9
	GSVMVTVMAGADDPFYHKLSELQOGR	29.2	30.6	28.2	1.1	0.9

FIGURE 2H (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6Hβ-3-H12-IR	OOUUUUUUJJJDPFYHKLSELXXOO	--	--	--	--	--
B6Hβ-3-G10-IR	RGEAKEAKIGSAGDPFYHKLSELMQGSR	33.6	32.0	29.5	1.1	0.9
B6Hβ-3-F10-IR	GCEVVVMANSSADPFYHKLSELCOGSR	30.1	34.3	30.5	1.1	0.9
B6Hβ-3-D5-IR	GCAAVVTTGGDNDPFYHKLSELLQGCR	37.1	35.3	32.4	1.1	0.9
B6Hβ-3-B12-IR	SRTGERQVVGSHADPFYHKLSELLSS	39.9	38.9	35.5	1.1	0.9
B6Hβ-3-D2-IR	GCKEVVETAHADDPFYHKLSELLQGCR	39.5	40.0	37.1	1.1	0.9
B6Hβ-3-D1-IR	RRITIKVKAGDDDDPFYHKLSELLWGG	40.4	41.5	39.1	1.1	0.9
B6Hβ-3-G6-IR	WCDQKETVVSNSDDPFYHKLSELVPCS	41.1	44.6	36.6	1.2	0.8
B6Hβ-3-A7-IR	RCEEITIGDGRAGDPFYHKLSELLQGC	34.3	36.4	24.1	1.5	0.7
B6Hβ-3-B10-IR	CSVVMTTEKNDRDDPFYHKLSELLQGC	38.1	30.9	18.4	1.7	0.6
B6Hβ-3-B9-IR	GGEARRRQQVGTANDPFYHKLSELAFGGR	32.3	36.5	22.8	1.6	0.6
B6Hβ-3-D6-IR	GCAVTAITINGTSDPFYHKLSELCOGS	38.6	38.5	20.8	1.9	0.5
B6Hβ-3-C7-IR	GSKVKAMAVGTSDDPFYHKLSELVQGR	35.9	36.0	15.6	2.3	0.4
	RCKGIKAHSDNDPFYHKLSELCOGG	38.3	38.0	6.6	5.8	0.2

FIGURE 2H (Con't)

Clone	Sequence	Ratios over Background		Comparisons	
Design		E-Tag	IGFsR	IR	IGFR/IR IR/IGFR
B6H-3-F1-IGFR	OOUUUUUUJJJJDPFYHKLSELLXXOO	--	-- --	--	--
B6H-3-D4-IGFR	RRVAAVA?KDATGDPFYHKLSELLRSG	20.0	30.8	--	--
B6H-3-G3-IGFR	RSTMKEKIEGDNDPFYHKLSELLKSG	19.0	27.6	--	--
B6H-3-F2-IGFR	GGAVIVTAARRGSDPFYHKLSELVGRG	14.2	25.2	--	--
B6H-3-D1-IGFR	SREAVEVTMARGSDPFYHKLSELVWGS	12.5	24.8	--	--
B6H-3-A3-IGFR	RSTTMVKAIVPPRPDPFYHKLSELL*GG	20.0	24.2	--	--
B6H-3-A4-IGFR	GRTEEVVVVGTRRDPFYHKLSELLASG	14.2	22.8	--	--
B6H-3-B4-IGFR	RRMAGWQ*TSSSDPFYHKLSELVSGS	13.0	22.8	--	--
B6H-4-D11-IGFR	SRKEVTEMVGGSPDPFYHKLSELMGSG	10.2	22.8	--	--
B6H-3-G2-IGFR	RGTAQRKSSDP*DPFYHKLSELIYGS	14.0	22.5	--	--
B6H-3-B2-IGFR	GGVVAVVAAGRRDDPFYHKLSELVSGR	15.2	22.5	--	--
B6H-3-E2-IGFR	SR.MAMVEVGNPGDPFYHKLSELLGS	14.5	21.9	--	--
B6H-3-B1-IGFR	RRVTAVIEVDGADDPFYHKL?ELLSGG	11.6	21.8	--	--
B6H-4-G3-IGFR	RSVIAN??G?NADPFYHKLSELISSG	15.9	21.7	--	--
B6H-4-F9-IGFR	RGVVIETTKDPGADPFYHKLSELLFGR	19.1	21.4	--	--
B6H-3-E3-IGFR	RRTTVMEIVGGRDDPFYHKLSELLHRG	11.3	20.9	--	--
B6H-3-E1-IGFR	GRVVAAAARPDPPDPFYHKLSELVAGR	14.2	20.8	--	--
B6H-4-F3-IGFR	RGVATVVVANHHSDPFYHKLSELVLRG	20.0	20.6	--	--
B6H-3-D2-IGFR	RRKMATEIMRSDADPFYHKLSELLGGS	12.5	20.3	--	--
B6H-4-A9-IGFR	GGKTAVEVTS PASDPFYHKLSELLLRG	12.1	19.3	--	--
B6H-4-E6-IGFR	RREKKVVTITDNDPFYHKLSELVFGG	14.1	19.2	--	--
B6H-4-C3-IGFR	SSAIIMVAADRADDPFYHKLSELLWGS	12.5	19.2	--	--
B6H-3-C2-IGFR	RRVAIVAAAGAGGDPFYHKLSELLSRG	23.6	18.9	--	--
B6H-3-C4-IGFR	RRMVMEAAENHADDPFYHKLSELLWRD	16.2	18.5	--	--
B6H-3-C3-IGFR	GRKMEIVAIRGAHDPFYHKLSELL*GR	16.8	17.2	--	--
B6H-3-B3-IGFR	CCIAMVEMAAGGGDPFYHKLSELLSGR	14.6	17.1	--	--
B6H-4-H3-IGFR	RGASQSPDPFYHKLSELAFGS	9.0	16.8	--	--
B6H-3-H3-IGFR	RKTAMVVI GDASDPFYHKLSELAFGS	10.1	16.6	--	--
	GSVITKAMKADGGDDPFYHKLSELL*GG	14.2	16.4	--	--

FIGURE 21

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
B6H-4-D8-IGFR	OOUUUUUUJJJJDPFYHKLSELXXOO	15.1	16.4	--	--
B6H-4-D6-IGFR	GGVKA AAAERDDSDPFYHKLSELFGS	12.6	15.6	--	--
B6H-4-E10-IGFR	CCEMVKTIEHGGNDPFYHKLSELVFR	10.2	15.1	--	--
B6H-4-F5-IGFR	GGAKVAVVDHGDDPFYHKLSELGRS	12.3	14.8	--	--
B6H-4-B2-IGFR	RGKTKMAAAGNRDPFYHKLSELI FGN	6.6	11.8	--	--
B6H-3-F3-IGFR	SGEGEMAMPGDDPFYHKLSELIGSRA	8.2	11.6	--	--
B6H-3-A2-IGFR	GGMAEVVVVGPPRDPFYHKLSELVGGG	10.9	9.9	--	--
B6H-3-H2-IGFR	GGEVKVMVADGSTDPFYHKLSEL LGRT	5.9	9.6	--	--
B6H-4-A1-IGFR	SCVMVETVAGNRDPFYHKLSELVGGC	4.4	9.5	--	--
B6H-3-H1-IGFR	RRW* KVPGAADPFYHKLSEL LGRSA	7.2	8.7	--	--
B6H-4-C2-IGFR	GGVEATEVEHADGDPFYHKLSELVGRS	6.7	8.6	--	--
B6H-4-H9-IGFR	RGVEVAVITHGPPDPFYHKLSEL LRG	12.3	8.4	--	--
B6H-4-B7-IGFR	SGTVTVIAMSGTDDPFYHKLSEL LRS	6.4	8.2	--	--
B6H-4-A7-IGFR	GRTAVVKEASPAHDPFYHKLSEL LRG	9.7	8.1	--	--
B6H-4-B3-IGFR	RGAIGNAAVGNRSDPFYHKLSELISRG	4.4	7.8	--	--
B6H-4-B4-IGFR	GGMIKTAMEHTRDPFYHKLSEL LRG	5.2	7.4	--	--
B6H-4-E1-IGFR	GCAEEVEVAGAGHDPFYHKLSEL CAGG	3.6	7.1	--	--
B6H-3-C1-IGFR	SSVVVVEVVDARRDPFYHKLSELV?SG	5.7	4.6	--	--
B6H-4-A3-IGFR	GRKKAVATMTDGGDPFYHKLSELILRS	4.4	4.2	--	--
B6H-4-H10-IGFR	RGETEMAVADTDDDPFYHKLSEL LRG	4.4	3.2	--	--
B6H-3-G1-IGFR	GQRDPFYHKLSELMGRGA	2.4	2.9	--	--

FIGURE 21 (Con't)



Clone	Design	Sequence	Ratios over Background			Comparisons		
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
B6C-3-C7-IR		EHWNTVDPFYHKLSELLRESG	31.7	2.1	20.0	0.1	9.4	
B6C-4-F2-IR		EHWNTVDPFYFTLFE*LRESG	8.2	1.8	4.3	0.4	2.4	
B6C-3-A2-IR		EHWNTVDPFYHQLSEWLRESG	34.9	18.1	36.0	0.5	2.0	
B6C-4-H11-IR		EHWNTVDPFYQQLYEWLRESG	37.1	28.2	38.6	0.7	1.4	
B6C-4-H4-IR		EHWNTVDPFYRQLSEWLRESG	39.5	28.3	39.4	0.7	1.4	
B6C-3-A11-IR		EHWNTVDPFYHYFQELLRESG	25.4	25.9	34.2	0.8	1.3	
B6C-3-D9-IR		EHWNTVDPFYHQMWEWLRESG	35.7	30.3	37.2	0.8	1.2	
B6C-4-G4-IR		EHWNTVDPFYRQLYEWLRESG	35.3	31.0	38.4	0.8	1.2	
B6C-3-C6-IR		EHWNTVDPFYHQLSEWLRESG	33.3	33.9	35.9	0.9	1.1	
B6C-3-D8-IR		EHWNTVDPFYH*ISELLRESG	34.5	34.7	37.1	0.9	1.1	
B6C-4-G7-IR		EHWNTVDPFYQFFAELLRESG	35.9	36.9	38.9	0.9	1.1	
B6C-3-C8-IR		EH*NTVDPFYEGLELLRESG	35.6	37.2	39.6	0.9	1.1	
B6C-3-D6-IR		EH*NTVDPFYQGLFELLRESG	37.6	37.6	40.2	0.9	1.1	
B6C-3-C10-IR		EHWNTVDPFYQYFSELLRESG	35.3	36.4	40.6	0.9	1.1	
B6C-3-B3-IR		EHWNTVDPFYHQLTLLRESG	38.3	38.7	40.8	0.9	1.1	
B6C-3-B1-IR		EHWNTVDPFYQALFELLRESG	37.8	38.9	41.2	0.9	1.1	
B6C-4-F6-IR		EHWNTVDPFYD*MRNLLRESG	35.8	36.8	38.7	1.0	1.1	
B6C-3-B11-IR		EHWNTVDPFYHQLQELLRESG	36.3	37.0	38.8	1.0	1.1	
B6C-3-B8-IR		EHWNTVDPFYDGLRQLRESG	37.2	39.2	41.2	1.0	1.1	
B6C-3-C12-IR		EHWNTVDPFYHQLQELLRESG	28.3	28.7	28.9	1.0	1.0	
B6C-3-C2-IR		EHWNTVDPFYQQLFELLRESG	34.1	34.7	33.8	1.0	1.0	
B6C-3-D5-IR		EHWNTVDPFYHQLQELLRESG	33.9	35.3	34.1	1.0	1.0	
B6C-4-F7-IR		EH*NTVDPFYHKLSELLRESG	34.9	34.7	34.2	1.0	1.0	
B6C-4-H2-IR		EHWNTVDPFYH*MSNLLRESG	35.4	35.8	35.8	1.0	1.0	
B6C-3-B12-IR		EHWNTVDPFY*MSNLLRESG	33.6	35.2	36.0	1.0	1.0	
B6C-3-A12-IR		EHWNTVDPFYHQLFELLRESG	33.1	37.0	36.2	1.0	1.0	
B6C-4-E9-IR		EHWNTVDPFYQRMFELLRESG	36.1	36.0	36.2	1.0	1.0	
B6C-4-E8-IR		EHWNTVDPFYQGLWELLRESG	34.2	35.0	36.6	1.0	1.0	

FIGURE 2J

**FIGURE 2J (Con't)**

01 02 03 04 05 06 07 08 09 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6C-4-F4-IR	EHWNTVDPPFYHKLSELLRESG	--	--	--	--	--
B6C-3-D2-IR	EHWNTVDPPFYQKLFELLRESG	36.3	36.9	34.3	1.1	0.9
B6C-3-A1-IR	EHWNTVDPPFYH*LAELLRESG	8.5	10.3	9.0	1.2	0.9
B6C-3-B5-IR	EHWNTVDPPFYH*LNELLRESG	26.5	30.7	16.8	1.8	0.5
B6C-3-A4-IR	EHWNTVDPPFYHKLQELLRESG	33.4	33.0	15.0	2.2	0.5
	EHWNTVDPPFYRRLLQELLRESG	33.6	31.8	13.5	2.4	0.4

FIGURE 2J (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
B6C-3-C4-IGFR	EHWNTVDPF <del>YHKLSELL</del> RESGA	--	--	--	--	--
B6C-3-F5-IGFR	EHWNTVDPFY <del>LKMT</del> ELLRESGA	21.0	23.1	--	--	--
B6C-3-D4-IGFR	EHWNTVDPFYH <del>KLE</del> ELLRESGA	26.5	22.6	--	--	--
B6C-3-A3-IGFR	EHWNTVDPFYH <del>KLYE</del> LLRESGA	26.6	22.1	--	--	--
B6C-3-C9-IGFR	EHWNTVDPFYQ <del>KLSELL</del> RESGA	29.7	20.8	--	--	--
B6C-3-C8-IGFR	EHW?TVDPFY <del>LKSELL</del> ?ESGA	29.6	20.5	--	--	--
B6C-3-A8-IGFR	EHWNTVDPFYQ <del>RLLFELL</del> RESGA	30.5	19.9	--	--	--
B6C-3-A2-IGFR	EHWNTVDPFYH <del>GLQELL</del> RESGA	29.7	19.7	--	--	--
B6C-3-A9-IGFR	EHWNTVDPFYH <del>RLLSELL</del> RESGA	33.6	19.0	--	--	--
B6C-3-C10-IGFR	EHWNTVDPFYH <del>NLYE</del> LLRESGA	33.0	18.3	--	--	--
B6C-3-F7-IGFR	EHWNTVDPFY <del>NKLSELL</del> RESSA	30.0	17.7	--	--	--
B6C-3-F10-IGFR	EHWNTVDPFYQ <del>KLSELL</del> RESGA	27.3	17.6	--	--	--
B6C-3-C12-IGFR	EHWNTVDPFYA <del>KLSALL</del> RESGA	27.4	17.4	--	--	--
B6C-3-E11-IGFR	EHWNTVDPFYA <del>RLSALL</del> RESGA	28.4	17.3	--	--	--
B6C-3-F8-IGFR	EHWNTVEP*YH <del>KLCGR</del> LLRESGA	28.0	17.2	--	--	--
B6C-3-F2-IGFR	EHWNTVDPFYD <del>RLLTE</del> LLRESGA	25.4	16.0	--	--	--
B6C-3-B6-IGFR	EHWNTVDPF*PK <del>VSELL</del> RESGA	30.8	15.1	--	--	--
B6C-3-D5-IGFR	EHWNTVEPFGA* <del>LAEP</del> LLRESGA	2.9	14.7	--	--	--
B6C-3-A4-IGFR	ERWNTVDPFYH <del>KLSSELL</del> RESGA	2.4	14.3	--	--	--
B6C-3-D3-IGFR	EHWNTVDQFYQ <del>ALFELL</del> RESGA	22.6	13.9	--	--	--
B6C-3-A7-IGFR	EHWNTVDPFYH <del>KLAELL</del> RESGA	28.0	13.8	--	--	--
B6C-3-H10-IGFR	EHWNTVDPFYD <del>KLSDDL</del> LLRESGA	24.8	13.6	--	--	--
B6C-3-H11-IGFR	EYWNTVDPFYH <del>KLAELL</del> RESGA	14.4	12.8	--	--	--
B6C-3-A1E-IGFR	EHWNTVRPRYQ* <del>LSELL</del> RESGA	17.1	11.1	--	--	--
B6C-3-E12-IGFR	EHWNTVATF*DK <del>VTDLL</del> RESGA	2.3	11.0	--	--	--
B6C-3-H12-IGFR	EHWNTVDPFLD <del>KRS*LL</del> RESGA	23.3	10.5	--	--	--
B6C-3-G1-IGFR	EHWNTVGA <del>FQPTPEYLL</del> RESGA	2.7	10.1	--	--	--
		2.3	9.9	--	--	--
		--	--	--	--	--

FIGURE 2K

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Design	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
Parental	FYDAIDQLVGRSARAGGTRD	30.6	15.1	4.2	3.6	0.3
20E2A-4-F9-IR	PPWGARFYDAIEQLVFDNLCC	19.9	1.2	13.9	0.1	11.5
20E2A-4-E2-IR	IGRVRSFYDAIDQLFQSDWER	13.9	1.3	9.7	0.1	7.6
20E2A-3-B6-IR	RDAGSSFYDAIDQLVCLTYFC	14.5	1.6	6.1	0.3	3.8
20E2A-3-A7-IR	MPMGLNFYDGIQLVREWGDD	18.6	4.2	15.2	0.3	3.6
20E2A-4-F7-IR	TISAHTFYEAIQYQIEGIDPL	20.1	10.6	15.8	0.7	1.5
20E2A-3-C9-IR	SPWGRAFYDALDQLMGAERG	24.4	16.4	23.8	0.7	1.4
20E2A-3-C11-IR	LSPPRDFYDAIQQLVVRDGGWG	14.8	5.9	6.6	0.9	1.1
20E2A-4-G7-IR	HGVPRTFYDAIDQLVWGIEVG	17.2	8.3	8.9	0.9	1.1
20E2A-4-H11-IR	GGTDQLFYGAIDQLVGGTWWR	25.4	26.9	25.6	1.1	1.0
20E2A-4-E9-IR	LSVHQSFYDAINEILFSGLEA	4.7	2.1	2.1	1.0	1.0
20E2A-4-F4-IR	GDARDPFYDAMEQLVYGEELGG	12.6	5.6	5.7	1.0	1.0
20E2A-3-A3-IR	VASPRSFYEAIAQLVFNLGQE	21.0	11.9	12.1	1.0	1.0
20E2A-4-E4-IR	RKPCQTFYDCILDLVVTDVDV	21.0	16.0	16.1	1.0	1.0
20E2A-4-G5-IR	LLSRWTFYDAIEQLVGGGADG	22.1	19.5	18.8	1.0	1.0
20E2A-4-H1-IR	PAGCQGFVEAIEQLVTGCECG	24.4	20.4	21.2	1.0	1.0
20E2A-3-D8-IR	AVFPRTFYEAIQQLVGVSLLG	22.3	20.8	20.3	1.0	1.0
20E2A-4-F11-IR	APIPFSFYDAIVQLVMQGDHE	23.2	21.0	20.4	1.0	1.0
20E2A-3-C1-IR	QCNPRTFYEIAIAQLVTGCDVS	23.4	22.3	22.5	1.0	1.0
20E2A-3-B2-IR	VSTSGSFYDAIQQLLEDSSGW	24.6	22.5	22.8	1.0	1.0
20E2A-4-G10-IR	HHSAFSFYDAIAQLVGVPEEE	21.5	22.9	22.2	1.0	1.0
20E2A-3-A5-IR	FTYVHSFYDAIEQLVVRGEGGG	24.6	23.4	22.6	1.0	1.0
20E2A-4-H3-IR	QGNNAQNFYDAIDQLCFGCLGG	24.5	24.1	25.1	1.0	1.0
20E2A-3-C4-IR	SSEGWTFFYDAIDQLVGRERGW	25.2	24.4	24.7	1.0	1.0
20E2A-4-E3-IR	PDGCATFFYHAIQQLVTGFPCV	18.5	15.7	13.6	1.2	0.9
20E2A-4-E7-IR	RGPPMTFFYDAIAQLVAQSADG	17.8	16.6	14.4	1.2	0.9

**FIGURE 2L**

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGF/IR	IR/IGF
20E2A-3-B3-IR	XXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-4-H10-IR	RSSCQSFYDAIERLVLGTCG	22.4	18.6	15.9	1.2	0.9
20E2A-4-F8-IR	VSRKFSFYDAIQQLVRGDAGV	24.8	24.5	21.2	1.2	0.9
20E2A-4-H5-IR	FQRTWSFYDAINQLVMEGSGD	4.3	2.2	2.1	1.1	0.9
20E2A-4-G1-IR	RGSATTFYDAINQLVGQDGGW	21.3	18.3	16.5	1.1	0.9
20E2A-4-F2-IR	AQPCVSFYDAIEQLVTGRSCM	21.4	18.3	16.0	1.1	0.9
20E2A-4-H7-IR	GGDGPFFYDWIEQLVRAGSEA	20.1	20.5	18.2	1.1	0.9
20E2A-3-D5-IR	LDLCASFYDAIEQLVGKFCG	22.6	21.2	18.6	1.1	0.9
20E2A-3-A1-IR	WLACQSFYDAIDQLINGECN	22.7	21.3	18.9	1.1	0.9
20E2A-4-H9-IR	EVNALSFYDAIDQLVRGGLGG	23.8	21.7	19.9	1.1	0.9
20E2A-3-D7-IR	RLQPRTFYEAIDQLIGVLEG	24.0	22.5	20.8	1.1	0.9
20E2A-4-E5-IR	SGAHRTFYDAIQELVGMGSK	24.1	23.5	21.0	1.1	0.9
20E2A-4-E11-IR	NMQSLTFYDAIAQLVLRSGG	24.1	23.5	20.9	1.1	0.9
20E2A-3-A4-IR	RAVGATFYDQINQLVRKDDGY	22.5	14.6	11.7	1.3	0.8
20E2A-4-G8-IR	SQCRGGFYDAIYQLVTGVNCI	20.2	17.5	13.4	1.3	0.8
20E2A-3-B7-IR	DRLAFSFYDAIDQLVHCCGHG	21.7	18.0	13.8	1.3	0.8
20E2A-4-G11-IR	GNRQGFYDAIDQLVGGSWWR	21.1	21.4	16.9	1.3	0.8
20E2A-3-C5-IR	GGSVLSFYDAIAQLVGGQSI	22.9	23.1	17.7	1.3	0.8
20E2A-4-E8-IR	RSGPMSFYDAIEQLVGLRHP	24.2	24.3	19.0	1.3	0.8
20E2A-4-H2-IR	VSGCRTFYDAIDQLVSGQACG	17.1	11.5	9.4	1.2	0.8
20E2A-4-H4-IR	AQFPRTFYDAIEQLIHGKMD	21.6	13.7	11.6	1.2	0.8
20E2A-3-D4-IR	CAQPESFYDAIDRLVTGRCLV	21.3	19.6	16.3	1.2	0.8
20E2A-4-F5-IR	PDECQSFYCAIDRLVTGKGR	23.2	22.2	18.0	1.2	0.8
20E2A-3-B10-IR	QRRARDFYEAIQQLVGGVAGL	12.2	5.7	3.8	1.5	0.7
20E2A-3-B9-IR	PLVRGTFYDAIKQLVMGSSD	14.9	5.9	3.9	1.5	0.7
20E2A-3-D10-IR	VGIATFYDAIQQLVRGSPEG	15.5	11.0	7.2	1.5	0.7
20E2A-3-D6-IR	PRQASFYDMIEQLVGSADWN	22.2	19.1	12.8	1.5	0.7
20E2A-4-G9-IR	DGRVWSFYDALEQLVGQFEGP	21.8	19.3	13.0	1.5	0.7
20E2A-4-E1-IR	RFVRSFYDAIEQLILAPNLG	21.3	19.9	13.3	1.5	0.7
20E2A-4-F12-IR	KVGRGSFYDAIRELVGQGHV	23.1	20.7	13.6	1.5	0.7
20E2A-4-G3-IR	PAIGFTFYDAIRQLVWFQCAD	17.5	17.1	12.1	1.4	0.7
	ALPGRSFYDAIAQLVGPDWGA	21.6	19.4	14.1	1.4	0.7

FIGURE 2L (Con't)

**FIGURE 2L (Con't)**

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
D sign	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
Parental	FYDAIDQLVRGSARAGGTRD	30.6	15.1	4.2	3.6	0.3
20E2A-4-F11-IGFR	QGSASFYDAIDRLRLMRIGG	21.3	18.8	1.3	14.6	0.1
20E2A-4-F12-IGFR	AQSGEGFYDALAQVLVQGVSG	23.3	23.9	3.1	7.8	0.1
20E2A-3-B4-IGFR	GHPAVSFYDAIDQLLRRRGGG	21.8	16.6	2.4	6.9	0.1
20E2A-4-F4-IGFR	YSDTYSFYDAIVQLVRRGASA	20.7	20.0	3.6	5.5	0.2
20E2A-3-C7-IGFR	VGTVAGFYDAIAQLVARASRV	17.6	5.4	1.1	5.1	0.2
20E2A-3-C10-IGFR	RFVWGSFYDAIDQLVQGRWRG	23.3	21.0	4.2	5.0	0.2
20E2A-3-D6-IGFR	RAVGDSFYEAIDQLVRRGGHV	15.1	11.8	2.4	5.0	0.2
20E2A-4-F6-IGFR	LRSQLSFYEAIDQLVQWKGA	21.5	19.9	4.3	4.6	0.2
20E2A-3-A8-IGFR	DKFSTSFYDAIDQLVQSVRGV	22.2	13.3	2.9	4.6	0.2
20E2A-4-F9-IGFR	MQSGFSFYDAIDRLVGRGLGER	21.2	19.0	4.4	4.4	0.2
20E2A-4-F3-IGFR	VGSSSFYEAIERLVQGLGRH	20.6	19.3	4.6	4.2	0.2
20E2A-3-B2-IGFR	LSWAAGFYEAIDQLVRSGGHR	18.7	14.7	3.8	3.9	0.3
20E2A-4-G8-IGFR	QQVHAGFYEAELVGFGLG	20.9	10.8	2.7	3.9	0.3
20E2A-3-D10-IGFR	MMVVDGFYDALHQLVVAQSLG	20.6	6.9	1.8	3.9	0.3
20E2A-3-A12-IGFR	LSVALSFYDALGQLVAGEGRW	16.1	4.3	1.1	3.9	0.3
20E2A-3-A11-IGFR	SGSNLGFYDALRQLVGATDGS	17.8	9.7	2.6	3.7	0.3
20E2A-4-H1-IGFR	PSGFLSFYEAIDQLVHGVRWF	20.8	14.5	4.1	3.5	0.3
20E2A-4-F7-IGFR	AFTPTSFYDAIEQLVQQLSPR	19.5	17.9	5.3	3.4	0.3
20E2A-3-D7-IGFR	VSSLRSFYDALDELVRRPFQ	22.0	18.3	5.6	3.3	0.3
20E2A-3-A9-IGFR	VSMPPSFYDALKQLVRGISEG	24.7	10.5	3.2	3.3	0.3
20E2A-3-A10-IGFR	IGVSRGFYDAIDKLVRDRGSP	26.3	15.4	4.8	3.2	0.3
20E2A-3-B11-IGFR	GRSLLSFYDLIDQLVQAGNGG	15.8	10.7	3.4	3.2	0.3
20E2A-3-D12-IGFR	GQRAQSFYEALEARLVCEGRCT	13.9	9.0	2.8	3.2	0.3
20E2A-4-H11-IGFR	CRFQGSFYDAIDLLVLGVRTC	22.8	17.5	5.7	3.1	0.3
20E2A-4-H5-IGFR	RWAFQSFYDAIDHLVNHREGH	20.1	16.6	5.5	3.0	0.3
20E2A-4-E11-IGFR	LPSSSGFYNAIQQLVCGHRGC	21.0	12.6	4.2	3.0	0.3

FIGURE 2M



Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2A-4-F2-IGFR	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-3-D4-IGFR	TGVFNDFYDALQQLVGRVRD	19.4	19.0	6.8	2.8	0.4
20E2A-3-B10-IGFR	YGSFETFYDAIDQLVRRGSQP	16.1	11.8	4.2	2.8	0.4
20E2A-4-E5-IGFR	RQLLDSFYEAIDQLVRSERP	24.0	14.3	5.3	2.7	0.4
20E2A-3-D5-IGFR	WPRGDPFYDAMEKLLSQGGGR	18.1	20.6	7.9	2.6	0.4
20E2A-4-G11-IGFR	PGLIQSFYDAIDQLVQRGN	15.1	9.3	3.6	2.6	0.4
20E2A-3-C12-IGFR	MNVFVSFYDAIDQLVCQIGC	20.7	3.3	1.3	2.6	0.4
20E2A-4-G5-IGFR	LDMIGGFYEAIDQLVSGSLAP	25.9	17.4	7.2	2.4	0.4
20E2A-3-D9-IGFR	RRPCNSFYDAIQLLVGGPCG	23.6	14.6	6.0	2.4	0.4
20E2A-4-F10-IGFR	FGRRSTFYDLIDQLVGQGRGT	19.8	12.3	5.1	2.4	0.4
20E2A-4-E2-IGFR	LRAPRSFYEAIYQLAQRPSVP	21.4	21.6	9.3	2.3	0.4
20E2A-4-E3-IGFR	VQRFSSFYDALDQLVGHGVWK	22.6	21.3	9.1	2.3	0.4
20E2A-3-C4-IGFR	PSARMGFYDLIDQLVGLVPGS	21.0	21.8	10.1	2.2	0.5
20E2A-3-C5-IGFR	SLQPHDFYDAIHRLVFHGGRF	23.5	17.4	7.8	2.2	0.4
20E2A-4-G12-IGFR	ERHGGSFYDAIAQLLQSDRSR	22.2	17.1	7.7	2.2	0.4
20E2A-3-C3-IGFR	YQPPGSFYDWIRELVAGPRRE	24.3	16.3	7.4	2.2	0.5
20E2A-4-E10-IGFR	FAHASSFYDAIDQLVAKCQSP	11.3	2.7	1.2	2.2	0.5
20E2A-4-E6-IGFR	AQSSSGFYEALYQLVWGRPG	22.3	22.6	10.8	2.1	0.5
20E2A-3-B7-IGFR	TTSGGSFYDAMYQLVWGDWRR	22.6	19.9	9.4	2.1	0.5
20E2A-4-D3-IGFR	ARGTAGFYAELERLVRGQDHG	23.0	16.6	7.9	2.1	0.5
20E2A-4-G4-IGFR	PRHAINFYDAIHQLVFGPRQ	20.5	15.7	7.6	2.1	0.5
20E2A-4-F1-IGFR	QSAHWSFYDAIERLVNMDTMP	22.6	14.5	7.0	2.1	0.5
20E2A-3-B9-IGFR	VGVVSSFYDAIDQLVWDRGS	19.6	19.9	9.8	2.0	0.5
20E2A-4-E7-IGFR	DTLIASFYDAIDQLVRLGRNQ	23.0	17.1	8.7	2.0	0.5
20E2A-4-B1-IGFR	FQGTQGFYDAIERLMRRGERP	26.4	22.1	11.5	1.9	0.5
20E2A-4-G1-IGFR	WADWGSFYDAIEQLVQRGGV	25.3	20.7	11.1	1.9	0.5
20E2A-4-E9-IGFR	EQLSCGFYDAIHQLVHGGGLG	23.1	17.9	9.5	1.9	0.5
20E2A-4-E8-IGFR	CGQRCSFYDAIDQLVGLPGA	22.6	17.7	9.3	1.9	0.5
20E2A-3-D11-IGFR	MMRVDFGYEAIIDRLVNEGQAT	17.2	8.6	4.6	1.9	0.5
20E2A-3-A3-IGFR	RQATSFYEAIDQLMGSGGV	16.1	6.1	3.2	1.9	0.5
20E2A-4-G7-IGFR	GHYFGSFYDAIDQLVAGMLPG	5.2	3.0	1.5	1.9	0.5
	PEGVQGFYDALAHLVGGSLFG	24.4	21.1	11.5	1.8	0.5

FIGURE 2M (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20E2A-4-G2-IGFR	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-4-G3-IGFR	IGVLGSFYDAIDQLVRQGNR	22.3	17.5	9.9	1.8	0.6
20E2A-3-B5-IGFR	RDVADGFYAAIEQLVRGQGL	21.2	12.3	6.9	1.8	0.6
20E2A-4-H4-IGFR	VRQAKSFYDAIDQLVRGALRG	24.0	22.7	13.3	1.7	0.6
20E2A-4-F8-IGFR	QVFRGSFYDAIDALVRWGGR	22.2	20.6	12.0	1.7	0.6
20E2A-3-A6-IGFR	VGAASFYDAIDQLVGWSPGS	17.3	17.9	10.7	1.7	0.6
20E2A-4-H12-IGFR	PSPVWSFYDAIQQLVRSQGR	23.8	23.7	15.0	1.6	0.6
20E2A-3-B12-IGFR	PVSATSFYDAINQLVRMGRG	25.1	23.5	14.2	1.6	0.6
20E2A-3-B8-IGFR	VMRRDRFYDAIEQLVGRIGV	27.6	21.9	13.6	1.6	0.6
20E2A-3-C8-IGFR	TTYVNSFYDALQQLLGGDADV	21.5	19.0	12.2	1.6	0.6
20E2A-4-H10-IGFR	LSNMITFYDAINQLVGHVQSL	23.2	17.7	11.4	1.6	0.6
20E2A-3-C9-IGFR	ASSRLSFYDAIEQLIKWSPGP	25.3	23.8	16.2	1.5	0.7
20E2A-4-H2-IGFR	WDLVDSFYDAIDQLVGQVRPG	25.4	21.8	14.6	1.5	0.7
20E2A-3-B6-IGFR	FAFVGSFYDALAQLVAQPPRS	21.8	20.1	13.0	1.5	0.6
20E2A-4-G9-IGFR	EDQPNFSFYDAIRQLVMGRLSP	20.3	18.1	11.8	1.5	0.7
20E2A-4-H6-IGFR	SVGPRSFYDAIDQLVGGAWVG	26.0	16.1	10.8	1.5	0.7
20E2A-4-H9-IGFR	KFRVYTFYDAIDQLVNQGRGR	21.9	19.6	13.9	1.4	0.7
20E2A-4-G10-IGFR	GRGWGSFYEAIDQLVRLGET	24.9	16.8	11.8	1.4	0.7
20E2A-3-A4-IGFR	FTSFHTFYDAIEQLVQGQGD	25.3	16.5	12.1	1.4	0.7
20E2A-3-A7-IGFR	AGSVTSFYDAMEQLVATGSA	16.8	2.5	1.8	1.4	0.7
20E2A-4-E12-IGFR	PRESFSFYDAIHQLVTGRVRS	26.0	24.9	19.3	1.3	0.8
20E2A-3-D1-IGFR	LGRADGFYDAIKQLVGADWGG	23.3	23.1	17.8	1.3	0.8
20E2A-3-C6-IGFR	RSGTWTFYDALELLVQSGSR	24.0	22.4	17.6	1.3	0.8
20E2A-3-D2-IGFR	PVVLFSFYDAIDQLVRKGLGP	23.7	21.7	17.2	1.3	0.8
20E2A-4-E8-IGFR	GRRRQTFYDALEQLVGGEALG	21.4	15.1	11.4	1.3	0.8
20E2A-4-G6-IGFR	AGPDMSFYDAIDQLVHCCGPF	18.4	13.6	10.4	1.3	0.8
20E2A-4-F5-IGFR	HGEKLSFYDAIAQLVGFIDGH	24.7	21.9	17.7	1.2	0.8
20E2A-3-C2-IGFR	GYTPVDFYDAIRQLVTGWPG	21.7	21.7	18.2	1.2	0.8
20E2A-4-H8-IGFR	FGGFSSFYDALDQLARGGSD	22.5	19.6	15.8	1.2	0.8
20E2A-3-A5-IGFR	VGIVRGFYEAIERLVGDTHGQ	24.4	18.5	15.1	1.2	0.8
20E2A-3-C11-IGFR	TPGGFSFYDAIQQLVDVLSDS	22.7	15.6	12.6	1.2	0.8
	TNAALTFYDAIEQLVRWGQRD	25.8	24.3	21.2	1.1	0.9

FIGURE 2M (Con't)

Clone	Sequence
<b>Design</b>	XXXXXXFYDAIDQLVXXXXXX
20E2A-3-C1-IGFR	GQSPLSFYDAIDQLVRAFPVG
20E2A-3-B3-IGFR	AGQLGGFYIAICQLVGVEYCT
20E2A-3-D8-IGFR	SAGPLSFYDAIAQLVGAWRL

	Ratios over Background			Comparisons	
	E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
1	--	--	--	--	--
2	23.4	22.4	20.5	1.1	0.9
3	21.0	17.0	14.8	1.1	0.9
4	22.0	19.7	19.6	1.0	1.0

**FIGURE 2M (Con't)**

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Parental	XXXXXXXXFYxxxhxxhxxxxxx FYDAIDQLVRGSARAGGTRD	--	--	--	--	--
20E2Bα-3-B3-IR	AGVNAGFYRYFSTLLDWDQ	30.6	15.1	4.2	3.6	0.3
20E2Bα-4-F12-IR	SVKEVQFYRYFYDLLQSESG	33.5	1.2	23.5	0.1	20.0
20E2Bα-3-B8-IR	IEVTQPFYDYFQQLRLRYGND	35.5	5.9	27.8	0.2	4.7
20E2Bα-3-D2-IR	VQCRADFYSYFACLVGRPGSR	39.3	18.2	36.5	0.5	2.0
20E2Bα-3-A5-IR	RNYPIGFYQFFHELVISGGG	42.6	19.7	26.7	0.7	1.4
20E2Bα-3-A3-IR	DLGNSFYGLRLRLVLQDAVG	36.9	22.7	24.5	0.9	1.1
20E2Bα-4-E9-IR	CKDQPDFYMGIKCLISGGGSV	39.9	33.5	35.5	0.9	1.1
20E2Bα-4-G8-IR	ACEGGSFYGCLQSLMSVESGN	32.8	29.6	28.6	1.0	1.0
20E2Bα-4-F9-IR	AVHEDGFYDMLRKLLSEGDS	37.5	30.5	30.9	1.0	1.0
20E2Bα-4-E7-IR	LARNEFYRYFEQLVFGDTG	35.6	32.5	31.1	1.0	1.0
20E2Bα-3-D5-IR	ATCASSFYAQLNCLLSDFDVM	36.0	31.6	31.2	1.0	1.0
20E2Bα-4-F7-IR	VQACQNFYDCINTLLLLDLGG	39.5	33.1	31.8	1.0	1.0
20E2Bα-3-B12-IR	IRGADQFYQFFRELLEGVGE	36.6	32.9	32.5	1.0	1.0
20E2Bα-3-A11-IR	RAGSRGFYEFFENLLRVGAGG	37.0	33.4	33.5	1.0	1.0
20E2Bα-3-B7-IR	AQRCADFYACIEELLAPGSR	36.9	34.9	34.2	1.0	1.0
20E2Bα-3-B5-IR	PGGEGFYQGLQRLILGADGG	40.4	37.1	36.3	1.0	1.0
20E2Bα-4-G1-IR	QKRSEAFYDWIADLLGQETSG	41.6	36.4	34.5	1.1	1.0
20E2Bα-4-G11-IR	WGLRDDFYRGIRCLVQWSEGC	38.5	28.9	26.5	1.1	0.9
20E2Bα-4-E10-IR	DSTVCGFYCRLAQLVAEGGSP	33.2	30.1	27.8	1.1	0.9
20E2Bα-4-F11-IR	QHSCRTFYDCIRVLMDDGQLG	35.4	30.5	28.0	1.1	0.9
20E2Bα-4-H11-IR	WSGNVDFYMYIRQLCGDVCS	32.5	29.5	28.0	1.1	0.9
20E2Bα-4-H3-IR	QTVHRDFYAALQDLLINDLGF	34.8	32.0	28.7	1.1	0.9
20E2Bα-4-H7-IR	SSGCQDFYSCMIQLVTTGGGD	38.7	34.9	30.5	1.1	0.9
		35.3	32.5	30.5	1.1	0.9

FIGURE 2N

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXFYXXhXXXXXXXXXX	--	--	--	--	--
20E2Ba-3-B6-IR	SGPMVGFYRGLFSLSPEDLQ	39.7	34.9	31.5	1.1	0.9
20E2Ba-3-D1-IR	LAEPDSFYNWIAQLLEGFAG	41.6	35.1	31.7	1.1	0.9
20E2Ba-3-A9-IR	FSGCDNFYSCIQSLWLPGGV	37.3	35.1	32.4	1.1	0.9
20E2Ba-3-C4-IR	QVFCDNFYHC IETLLGVGQTP	39.6	36.3	33.4	1.1	0.9
20E2Ba-4-F3-IR	RGRDNQFYHGLWALLGSGLE	37.5	36.6	33.6	1.1	0.9
20E2Ba-4-F4-IR	VSGRGGFYDAIRDLIGPRDQG	37.2	36.9	33.7	1.1	0.9
20E2Ba-3-D4-IR	PVVLDDFYVALCQLMVQGDCE	42.1	38.0	34.5	1.1	0.9
20E2Ba-4-E4-IR	PDIADPFYAFFQGLLRADTPI	40.6	38.4	35.5	1.1	0.9
20E2Ba-4-G10-IR	VAQCTDFYACIRSLVRSGSPG	32.9	31.3	27.1	1.2	0.9
20E2Ba-3-D11-IR	CSQLVSFYLGMDCLLGRGGTQ	34.0	32.5	27.9	1.2	0.9
20E2Ba-3-C8-IR	PLACADFYQCLSDLRGGPAW	39.2	33.0	28.2	1.2	0.9
20E2Ba-4-F2-IR	VVICTGFYDCIYQLVGSHEEM	38.7	37.6	32.3	1.2	0.9
20E2Ba-4-H12-IR	CVDRRTFYEGLQCLLGGATGD	32.3	30.4	25.8	1.2	0.8
20E2Ba-4-E1-IR	VNLRDPFYQWIEALMDSAGGE	39.2	40.2	32.3	1.2	0.8
20E2Ba-4-H8-IR	LTSSTSFYDALFCLAGLQLCG	37.6	34.8	27.0	1.3	0.8
20E2Ba-3-B4-IR	DFDSSPFYRGLRQLLESRSFP	39.9	34.9	25.9	1.3	0.7
20E2Ba-4-E2-IR	HEAGWTFYDAIQCLVGGWCSK	38.8	36.3	23.5	1.5	0.6
20E2Ba-4-H1-IR	CQQWRSFYHAVSCLLGPDDPD	40.8	33.6	20.2	1.7	0.6
20E2Ba-3-A10-IR	MVDRDPFYQGLRDLIGRQKKG	32.8	32.6	18.5	1.8	0.6
20E2Ba-3-D3-IR	LGRGGFYRGLQDLIGTQWPR	41.9	29.5	5.6	5.3	0.2

FIGURE 2N (Cont.)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFsR/IR	IR/IGFsR
20E2Bβ-4-F7-IR	XXXXXXXXFYXXhxxhXXXXXXXX	--	--	--	--	--
20E2Bβ-3-E12-IR	DALNLRFYSYFQHLMEDQVTD	26.8	3.0	24.2	0.1	8.0
20E2Bβ-4-F3-IR	GNSGGSFYRYFQLLDSDGMS	17.2	1.4	5.5	0.3	4.0
20E2Bβ-4-F6-IR	GDRVPGFYDWIRQLMVDPLEV	25.2	2.0	7.7	0.3	3.9
20E2Bβ-3-D11-IR	SEREDPFYRWIQAMVEGVSEG	25.7	3.8	11.0	0.4	2.9
20E2Bβ-3-E5-IR	GSVACDFYCHMWSLVEQPAGT	14.8	3.6	4.2	0.9	1.2
20E2Bβ-3-C9-IR	VHPSAGFYKGLLALIGDSQLG	24.3	6.9	4.3	1.6	0.6
20E2Bβ-3-C7-IR	FCGGLSFYGCQLQELLTWESPT	29.7	24.3	15.0	1.6	0.6
20E2Bβ-4-H8-IR	QSGSGDFYDWLSRLIRNGDGG	1.5	3.1	1.5	2.0	0.5
20E2Bβ-4-G7-IR	LPRQDGFYDALRRLISEGAGG	25.8	26.9	13.2	2.0	0.5
	LQPCSGFYECIERLIGVKLSG	19.9	25.2	1.6	15.8	0.1

FIGURE 2N (Con't)

Clone	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	--
Design	XXXXXXXXXXXXXXXXXXXX	--	----	--	--	--	--
20E2B-1-A6-IGFR	GVRAMSFYDALVSVLGLPSG	18.6	18.1	1.1	16.8	0.1	1.1
20E2B-3-C6-IGFR	VEGRGLFYDLLRQLLARRQNG	17.9	16.8	1.1	14.8	0.1	1.1
20E2B-4-H3-IGFR	KLHNLMPFYGLQRLVWGAGLG	11.2	14.8	1.1	13.9	0.1	1.1
20E2B-3-C2-IGFR	GNGDGMFYQLLSLLVGRDMHV	13.1	8.9	0.6	13.8	0.1	1.1
20E2B-3-E3-IGFR	PDLHKGFYAQLALIRGQLLS	22.4	16.3	1.3	13.1	0.1	1.1
20E2B-4-H12-IGFR	YSCGDGFYSLLSDLLGGQFRC	6.5	9.7	0.8	12.8	0.1	1.1
20E2B-3-D2-IGFR	IQQLTFYDLLHRLVRSELGS	20.7	12.4	1.1	11.7	0.1	1.1
20E2B-3-D8-IGFR	GGTEVDIFYRALERLVRGQLGL	20.4	17.7	1.6	11.3	0.1	1.1
20E2B-3-E8-IGFR	LRIANLFYQRLWDLAFGGGG	15.7	16.7	1.5	11.1	0.1	1.1
20E2B-4-F8-IGFR	PVGVGQFYEGLSRLVLGRGWW	12.3	7.3	0.8	9.7	0.1	1.1
20E2B-1-A11-IGFR	RFSTDGFYQYLLALVGGGPVG	15.0	9.5	1.0	9.7	0.1	1.1
20E2B-3-D4-IGFR	NSRDGGFYQLERLLGFPVTG	8.1	7.9	0.8	9.6	0.1	1.1
20E2B-2-B11-IGFR	VVTPVNFYRALEALVRGQRLG	13.9	10.6	1.1	9.4	0.1	1.1
20E2B-3-C8-IGFR	QPAPDGFYSALMKLIGRGVS	18.5	15.6	1.8	8.9	0.1	1.1
20E2B-2-B2-IGFR	PGTDLGFYQALRCVVIQGACD	11.7	4.9	0.6	8.1	0.1	1.1
20E2B-4-F10-IGFR	AQPCGGFYGLLEQLVGRSVCD	19.0	17.3	2.2	7.8	0.1	1.1
20E2B-4-F9-IGFR	QPDHSFYFYSLLQELVGSERL	11.9	14.7	1.9	7.7	0.1	1.1
20E2B-3-D11-IGFR	LGVTDFGYAALGYLIHVGQF	14.3	12.2	1.6	7.6	0.1	1.1
20E2B-3-C11-IGFR	CMMQDGFYAGLGCLLTAGEGR	15.3	15.4	2.1	7.5	0.1	1.1
20E2B-2-B3-IGFR	ICTGGQFYQVLCGLLRGTSAR	9.1	5.3	0.7	7.4	0.1	1.1
20E2B-3-D12-IGFR	QGNVLDIFYGWI GRLLAKQGS D	10.3	6.2	0.9	7.3	0.1	1.1
20E2B-3-E12-IGFR	VATSQGFYSGLSELLQGGNV	13.9	6.0	0.8	7.3	0.1	1.1
20E2B-2-B8-IGFR	IWATGDFYRLLSQLVMG RVGT	17.4	5.7	0.8	7.2	0.1	1.1
20E2B-4-G11-IGFR	RQGTGSFYLMLEQLLLVGARGP	8.9	4.5	0.6	7.0	0.1	1.1
20E2B-3-D6-IGFR	DSVGNFYLQLESLLVGGHVG	20.7	17.8	2.6	6.9	0.1	1.1
20E2B-2-B7-IGFR	LSSDQQFYRALNLLLQGSAGR	18.0	6.1	0.9	6.7	0.1	1.1
20E2B-3-C4-IGFR	ASSASGFYELLQRLAGLGLEV	23.4	20.4	3.3	6.2	0.2	1.1

Clone	Sequence	Genomic Data				Comparisons			
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	IR/IGFR	IR/IGFR	
Design	XXXXXXXXFYXXhXXXXXXXX	--	--	--	--	--	--	--	
20E2B-3-D3-IGFR	CGRRDPYGGIICLLGQKGVV	21.0	16.1	2.6	6.2	0.2	0.2	0.2	
20E2B-4-H8-IGFR	PAGPCGYCGLGLLLHGDQSP	7.2	5.3	0.9	5.9	0.2	0.2	0.2	
20E2B-3-E9-IGFR	QAAPQDFYQGLWLLIHRDPTM	14.7	16.2	2.8	5.8	0.2	0.2	0.2	
20E2B-4-H9-IGFR	RCQGTGYTCIQELIGFGDPD	4.5	5.2	0.9	5.6	0.2	0.2	0.2	
20E2B-1-A8-IGFR	TLRSPTFYDWLEMLVTHGQGG	16.1	4.4	0.9	5.0	0.2	0.2	0.2	
20E2B-4-H11-IGFR	STHSRAFYDAIAQLVGSVLGP	10.7	11.0	2.3	4.8	0.2	0.2	0.2	
20E2B-3-C9-IGFR	RQGGSFYELLCGLVGGEVCV	17.9	19.7	4.2	4.6	0.2	0.2	0.2	
20E2B-3-E6-IGFR	RQASGFYRALHDLMLRTQDY	24.5	21.6	4.7	4.6	0.2	0.2	0.2	
20E2B-3-E11-IGFR	SRANLIFYMGLSQLLLRNRGL	16.5	7.7	1.9	4.1	0.2	0.2	0.2	
20E2B-4-G8-IGFR	GRALDPFYDQLRDLVARSGGG	11.1	14.9	3.7	4.1	0.2	0.2	0.2	
20E2B-4-H10-IGFR	EASCRTFYCGLMALIGDDQR	2.2	2.5	0.8	3.1	0.3	0.3	0.3	
20E2B-3-E7-IGFR	QNGCKDFYCLIDNLIRYPGG	14.4	8.8	3.0	3.0	0.3	0.3	0.3	
20E2B-3-C12-IGFR	QHSRCTFYDCIRVLMDDGQLG	6.2	6.4	2.2	2.9	0.3	0.3	0.3	
20E2B-4-G12-IGFR	LDSRRGFYDWIKALIGDRDVQ	9.6	10.0	3.8	2.6	0.4	0.4	0.4	
20E2B-4-G3-IGFR	CQQKGFYAGLVCLLRERASQ	27.2	23.8	9.1	2.6	0.4	0.4	0.4	
20E2B-3-E4-IGFR	GGSQSFYDVMCMLLQLDPTC	24.9	22.3	8.9	2.5	0.4	0.4	0.4	
20E2B-3-E2-IGFR	VESDVSFYEGLMRLVVMWGQGG	18.6	20.2	8.7	2.3	0.4	0.4	0.4	
20E2B-2-B4-IGFR	ERAGDLFYQWFERLVVAGHGLE	5.8	2.3	1.0	2.2	0.5	0.5	0.5	
20E2B-3-C5-IGFR	RMPSGSFYQGIYELVTRQGGF	6.3	2.0	0.9	2.2	0.5	0.5	0.5	

**FIGURE 20 (Con't)**



Clone ID	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR
Design	XXXXXXXXFYRYFXXLLXXXXXXXX	--	--	--	--	--
NMRPβ-4-G6-IR	RWPNFYGYFESLLTHFS	10.1	1.9	20.1	0.1	10.6
NMRPβ-4-F3-IR	HYNAFYEFQVLLAETW	8.6	1.3	13.6	0.1	10.5
NMRPα-2-C1-IR	EGWDFYSYFSGLLASVT	19.7	2.0	10.9	0.2	5.3
NMRPα-4-E1-IR	LDRQFYRYFQDLLVGFM	11.5	6.5	21.2	0.3	3.2
NMRPα-3-H6-IR	WGRSFYRYFETLLAQGI	19.1	2.1	6.0	0.3	2.9
NMRPβ-4-F7-IR	RREGFYHYFQSLLEYG	0.7	0.9	2.3	0.4	2.7
NMRPα-2-D1-IR	GGGQFYRYFIDMLVLDI	18.4	1.5	3.7	0.4	2.5
NMRPα-1-A1-IR	PTGPFDRYFARRLVWRG	15.2	1.3	3.1	0.4	2.4
NMRPα-2-C10-IR	RGGAFYRYFEGLLSQHN	18.8	3.8	8.8	0.4	2.3
NMRPα-3-G1-IR	WRDPFYRYFQDLLLEGER	18.9	4.2	8.6	0.5	2.1
NMRPα-4-C3-IR	WGGEFYRYFVQLLSSED	17.9	12.9	25.7	0.5	2.0
NMRPα-4-D1-IR	GRESFYGYFLDLLQETV	16.2	12.7	23.2	0.5	1.8
NMRPβ-4-F4-IR	GHAEFYGYFQGLLDSYL	19.5	16.0	25.6	0.6	1.6
NMRPα-1-B2-IR	GGEAFYRYFWGLLTEWE	14.8	8.4	12.9	0.7	1.5
NMRPα-1-B4-IR	LSSGFYRYFTGLLSDGQ	19.1	6.3	9.2	0.7	1.5
NMRPα-4-D9-IR	DPGAFYRYFAQLMDTWN	7.6	16.9	25.7	0.7	1.5
NMRPβ-4-F2-IR	KHEQFYVEYFRNLLGAMS	21.6	20.9	30.8	0.7	1.5
NMRPβ-4-H12-IR	RDGAFYRYFEDLLIAVD	5.2	13.8	20.0	0.7	1.5
NMRPα-4-E7-IR	RGNRFYEFYELLRDYG	9.4	21.9	29.7	0.7	1.4
NMRPα-1-B5-IR	ELGDFYRYFQLLLADWH	14.1	5.4	7.1	0.8	1.3
NMRPα-4-C4-IR	AQDAFYSYFSVLLGEHL	17.6	17.6	22.3	0.8	1.3
NMRPα-4-C7-IR	IGVNFYRYFEKLLLEDEF	4.5	11.2	14.9	0.8	1.3
NMRPα-4-D3-IR	TDSQFYSYFESLLETFG	16.4	13.5	17.9	0.8	1.3

**FIGURE 2P**

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR
NNRPβ-4-G10-IR	XXXXXXXXFYRYFXLLXXXXXXXX	8.8	8.7	11.7	0.7	1.3
NNRPβ-4-H2-IR	SSREFYSYFSGLLTAL	4.9	19.9	25.3	0.8	1.3
NNRPα-4-C1-IR	TGRGFYRYFEGLLDWM	15.5	18.0	21.1	0.9	1.2
NNRPα-4-C5-IR	SGSWFYRYFEELLQSG	18.0	23.3	26.9	0.9	1.2
NNRPα-4-C6-IR	GRGGFYQYFLDLLQTEA	7.8	13.6	15.7	0.9	1.2
NNRPα-4-C12-IR	GQNGFYRYFDTLADWV	12.3	16.7	19.9	0.8	1.2
NNRPα-4-D7-IR	FAGSFYRYFEQLLSEQ	10.2	23.7	27.9	0.8	1.2
NNRPα-4-D11-IR	DPNAFYRYFEGLLWREH	5.4	19.3	22.3	0.9	1.2
NNRPβ-4-F1-IR	?GLNFYRYFVGLLTDTL	21.7	23.0	28.6	0.8	1.2
NNRPβ-4-F9-IR	RHINFYGYFDDLLATWH	10.1	18.4	22.5	0.8	1.2
NNRPβ-4-F12-IR	FHRGFYRYFINLLSGDA	4.5	13.5	16.6	0.8	1.2
NNRPγ-4-A3-IR	MGSSFYRYFETLLGQGL	16.4	22.3	26.8	0.8	1.2
NNRPα-1-A7-IR	GSLDFYSYFWERLGLGP	16.9	1.2	1.3	0.9	1.1
NNRPα-4-C11-IR	STVSFYRYFYALLQSPC	7.8	19.7	21.2	0.9	1.1
NNRPα-4-D8-IR	LGGYFYRYFEDLLNHQS	6.9	17.6	20.1	0.9	1.1
NNRPα-4-D10-IR	DHRGFYRYFLYQLAGNV	6.4	17.2	19.5	0.9	1.1
NNRPα-4-E5-IR	EYSGFYGYFNHLLGSLG	13.2	26.1	27.6	0.9	1.1
NNRPα-4-E8-IR	TSNWFYQYFTDLLAGED	8.7	22.9	24.2	0.9	1.1
NNRPα-4-E10-IR	SSGGFYRYFSQLLTEMN	3.5	12.4	13.2	0.9	1.1
NNRPβ-4-F8-IR	VHGEFYRYFESLLRETF	8.1	22.9	25.2	0.9	1.1
NNRPβ-4-F10-IR	SDEGFYRYFAQLLYGVT	5.3	17.9	19.1	0.9	1.1
NNRPβ-4-G8-IR	ETGGFYGYFQALLATYH	10.6	27.2	28.9	0.9	1.1
NNRPβ-4-H3-IR	GDRGFYRYFEWLLNDFG	3.9	24.2	25.7	0.9	1.1
NNRPβ-4-H9-IR	FGGAFYRYFEALLGEMG	4.1	26.5	29.3	0.9	1.1
NNRPβ-4-H10-IR	DGGAFYRYFEALLGELD	3.4	22.3	24.6	0.9	1.1
NNRPγ-4-A6-IR	WHSDFYRYFLLSLQEDG	14.9	25.8	27.6	0.9	1.1
NNRPγ-4-A8-IR	EEEGFYGYFYRLLGVER	9.8	22.8	24.7	0.9	1.1
	MDAGFYGYFSDLLANWG					

FIGURE 2P (Con't)



Clone	Sequence	E-Tag	IGFR	IR	IGFR/IR	IR/IGFR
Design	XXXXXXXXFYRYFX <del>XXXXXXXX</del>	--	--	--	--	--
NRPγ-4-A12-IR	AFYRYFRDLLFSGF	4.9	16.3	14.9	1.1	0.9
NRPγ-4-B8-IR	DDRGFYRYFESLLLGSS	6.1	21.3	19.9	1.1	0.9
NRPα-1-A5-IR	LSTSFYQYLAGLLRGDR	2.3	1.4	1.1	1.2	0.8
NRPα-1-B7-IR	GSSGFYRYFNMLML <del>SQT</del>	19.2	15.7	12.4	1.3	0.8
NRPα-2-C7-IR	GDRGFYRYFEGLLASVG	19.6	20.0	16.5	1.2	0.8
NRPα-2-C11-IR	NSAAFYRYFEQLLEREV	20.1	20.0	16.3	1.2	0.8
NRPα-2-C12-IR	LSDGFYRYFEQLMGARS	14.3	10.1	8.5	1.2	0.8
NRPα-2-D12-IR	RSTLFYRYFQNLLEE <del>VG</del>	11.5	11.4	9.3	1.2	0.8
NRPα-3-G2-IR	TRGGFYRYFEDLLQVYS	20.8	20.7	16.1	1.3	0.8
NRPα-3-G8-IR	GVS <del>GFYRYFQSL</del> DSYG	14.7	11.0	9.2	1.2	0.8
NRPα-3-G10-IR	QNDAFYSYFNSLLQAYT	18.8	16.5	13.9	1.2	0.8
NRPα-3-G11-IR	RQQDFYRYFRQLLEE <del>V</del>	12.0	10.3	8.5	1.2	0.8
NRPα-3-G12-IR	EGSGFYRYFEKLLQSP	11.7	11.8	9.3	1.3	0.8
NRPγ-4-B2-IR	RHKAFYRYFEELLQKNV	22.8	30.3	25.3	1.2	0.8
NRPα-1-B8-IR	GRMTRLIVRSTVISRELLHYS <del>L</del>	16.1	10.1	6.9	1.5	0.7
NRPα-2-C5-IR	QALSFYRYFERLLDEVS	18.1	19.2	13.7	1.4	0.7
NRPα-2-C9-IR	SKSAFYRYFDELLGNSG	22.9	21.7	16.1	1.3	0.7
NRPα-2-D2-IR	LGGAFYRYFAQLNSHV	26.1	26.2	17.6	1.5	0.7
NRPα-2-D5-IR	LNSGFYGYFVQLLSGHQ	21.7	21.1	15.4	1.4	0.7
NRPα-2-D11-IR	SQSSFYRYFESLLEDNP	12.3	10.8	7.8	1.4	0.7
NRPα-3-E2-IR	ADGGFYGYFAALLGSVS	24.4	25.5	18.3	1.4	0.7
NRPα-3-E4-IR	QNGSFYRYFIALLGDSG	23.0	22.3	14.7	1.5	0.7
NRPα-3-F4-IR	WDTGFYRYFIELLED <del>RD</del>	24.9	25.1	17.6	1.4	0.7
NRPα-3-G4-IR	HPRDFYRYFERLLNQVD	20.9	20.4	14.1	1.5	0.7
NRPα-3-H4-IR	DGGAFYRYFMDLLGAHE	17.7	17.6	11.6	1.5	0.7
NRPα-4-E12-IR	AGRGFYRYFEHLLAGRE	4.3	15.4	10.8	1.4	0.7
NRPβ-4-G11-IR	SSRGFYRYFRELLADSW	6.6	18.4	13.1	1.4	0.7
NRPβ-4-H6-IR	KYSGFYEYFNALLGRRE	2.2	16.1	11.7	1.4	0.7

**FIGURE 2P (Con't)**

Clone Design	Sequence	E-Tag	IGFR	IR	IGFR/IR	IR/IGFR
NNRPβ-4-H11-IR	XXXXXXFYRYFXLLXXXXXX	--	--	--	--	--
NNRPα-1-B1-IR	DYTA FYGYFNNLLRTSG	2.3	12.4	9.0	1.4	0.7
NNRPα-2-D7-IR	FQSSFYGYFESLLMSYK	18.8	18.7	11.5	1.6	0.6
NNRPα-2-D8-IR	DTNA FYRYFEGLLWSEH	21.0	21.8	13.2	1.6	0.6
NNRPα-3-E1-IR	GGSSFYRYFEQLLAQWE	20.2	19.8	12.2	1.6	0.6
NNRPα-3-E5-IR	SQGGFYRYFEKLLDEVT	20.0	20.5	12.9	1.6	0.6
NNRPα-3-H3-IR	RSGLFYRYFEELLQGA I	20.0	24.5	15.5	1.6	0.6
NNRPα-3-H5-IR	QGGFYHYFLSLLLEV G	19.8	19.1	12.2	1.6	0.6
NNRPα-1-A3-IR	WRGA FYRYFQTLSD EG	19.9	18.0	11.1	1.6	0.6
NNRPα-3-E6-IR	AAGFYGYFYSLLGDQT	24.4	14.9	7.9	1.9	0.5
NNRPα-3-F9-IR	RNSGFYRYFQHLVSEWE	23.1	19.0	9.6	2.0	0.5
NNRPα-3-G6-IR	QHR LFYSYFAELLGRDT	21.1	18.8	9.6	1.9	0.5
NNRPα-3-H9-IR	QID EFYRYFADQLRGFA	22.4	17.7	9.0	2.0	0.5
NNRPα-1-A8-IR	LGGFYRYFNLLVMGSG	18.3	13.1	6.9	1.9	0.5
NNRPα-1-A9-IR	GDRA FYRYFQRQLEGWG	16.9	13.8	5.7	2.4	0.4
NNRPα-2-D6-IR	CEDAFYRYFVNLLGQGC	16.5	15.2	5.6	2.7	0.4
NNRPα-3-F6-IR	NYSQFYRYFEMLLLEGDV	19.4	18.5	6.8	2.7	0.4
NNRPα-3-H2-IR	VGDA FYRYFQGLLRQDQ	22.8	19.5	7.9	2.5	0.4
NNRPα-1-B6-IR	MHGSFYRYFQDLLQAPP	19.9	18.9	8.5	2.2	0.4
NNRPα-2-C6-IR	DVGDFYRYFGLLLTSDR	14.1	11.5	3.9	3.0	0.3
NNRPγ-4-A1-IR	NSAAFYGYFSQLAQIR	18.4	19.2	4.1	4.7	0.2
NNRPγ-4-A7-IR	IIGGFYSYFNSVLRGT	9.7	10.9	1.8	6.0	0.2
NNRPγ-4-A9-IR	RFDPFYSYFVNLLGASA	2.5	6.3	1.3	4.9	0.2
NNRPγ-4-B11-IR	EGSGFYGYFFSLLGLQG	3.0	10.0	1.4	7.1	0.1
	LKDGFDYDFWQRLHLGS	4.1	18.7	1.2	15.5	0.1

FIGURE 2P (Con't)

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
<b>Design</b>	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20-4-F9-IGFR	PLAELWAYFEHSEQGRSSAH	33.1	19.3	1.0	19.3	0.1
R20-4-H4-IGFR	PVLSGLLRYFAGG <u>PL</u> GQPQS	24.1	5.6	3.2	1.8	0.6
R20-4-F9-IGFR	GGYLDLWHYFRDGQA <u>L</u> QPW	2.5	2.4	1.4	1.7	0.6
R20-4-D6-IGFR	VDQRQGGWLLALENYFRSTV	6.1	2.9	1.9	1.5	0.7
R20-4-G2-IGFR	DVPAGGLLRQMWVYFRSDP	6.3	2.2	2.0	1.1	0.9

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
<b>Design</b>	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20-4-F9-IGFR	PLAELWAYFEHSEQGRSSAH	33.1	19.3	1.0	19.3	0.1
R20-4-H4-IGFR	PVLSGLLRYFAGGPLGQPQS	24.1	5.6	3.2	1.8	0.6
R20-4-F9-IGFR	GGYDDLWHYFRDGGALQPW	2.5	2.4	1.4	1.7	0.6
R20-4-D6-IGFR	VDQRQGGWLLALENYFRSTV	6.1	2.9	1.9	1.5	0.7
R20-4-G2-IGFR	DVPAGGLLRQMWVYFRSDP	6.3	2.2	2.0	1.1	0.9

**Figure 3A**

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
<b>Design</b>	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
20C-3-F3-IGFR	RRVACTQADGLLCESDPLKALLSYF	35.5	32.8	17.9	1.8	0.5

## Design

20C-3-F3-IGFR

XXXXXXXXXXXXXXXXXXXX

RRVACTQADGLLCESDPLKALLSYF

	Ratios over Background		Comparisons	
	E-Tag	IGFsR	IGFR/IR	IR/IGFR
IR	--	--	--	--
IGFR	35.5	32.8	17.9	1.8
IGFR/IR				0.5



# Sequence

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
rB6-4-E7-IR	xxxLxxLxxYfxxxxx	--	--	--	--	--
rB6-4-A12-IR	LDPLDALLQYFWSVPGH	26.4	1.0	15.5	0.1	15.5
rB6-3-E6-IR	LDALDRLMRYFEERPSL	34.9	1.0	12.0	0.1	12.0
rB6-4-E11-IR	ADELEWLLDYFMHQPRP	9.0	1.0	4.8	0.2	4.8
rB6-4-F12-IR	DQELGWLGRGYFEWTARD	31.2	1.6	5.9	0.3	3.7
rB6-4-D11-IR	DGVLEELFSYFSATVGP	30.4	1.0	3.4	0.3	3.4
rB6-4-A8-IR	PMNLSELWDYFRLKPGR	41.9	15.7	30.2	0.5	1.9
rB6-4-E8-IR	DSILRELRDYFAPYSHC	25.6	2.4	4.6	0.5	1.9
rB6-4-B9-IR	DDALEWLLNYFQNGHVQ	33.0	9.7	15.9	0.6	1.6
rB6-3-A6-IR	GDILDALRLRYFEFGVDT	42.7	17.2	21.7	0.8	1.3
rB6-4-C7-IR	GDQLAWLLAYFQSDGSD	32.3	2.9	2.8	1.0	1.0
rB6-4-H12-IR	DGVLEGLLSYFTSTNSH	31.4	2.6	2.3	1.1	0.9
rB6-3-C6-IR	ARPLDWLLDYFKQGARG	26.0	10.0	7.2	1.4	0.7
rB6-4-G12-IR	DDMLRQLWLRYFEASAGG	34.2	19.1	12.8	1.5	0.7
rB6-4-G12-IR	DPWLAWLGRYFGETATG	37.7	6.1	3.1	2.0	0.5
rB6-4-C11-IR	DPTLFGLRLRYFQESGIA	33.3	7.6	3.5	2.2	0.5
rB6-4-G8-IR	MDPLRGLLMYFSQGLV	26.6	18.7	4.7	4.0	0.3
rB6-4-B8-IR	DGLLWQLWDYFALSEHR	37.3	7.4	1.3	5.7	0.2
rB6-4-D7-IR	DNWLSALMAYFMGSGES	31.1	28.6	1.0	28.6	<0.1
	DDVLNYLLGYFRQSDGL	24.1	29.4	1.0	29.4	<0.1

Figure 3C





Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXLYYFXXXXXX	--	--	--	--	--
rB6-3-F1-IGFR	NTILGDLWRYFAGSGGM	26.5	5.8	1.4	4.1	0.2
rB6-4-B7-IGFR	?DVLKKL?VYFELSGGA	31.1	11.4	2.9	3.9	0.3
rB6-4-C10-IGFR	GGPLQGLYTYFKQSPVC	32.2	3.7	1.0	3.7	0.3
rB6-3-A1-IGFR	DRLLSGLWAYFAGNGGS	21.1	3.5	1.0	3.5	0.3
rB6-3-F6-IGFR	DLILQSLLDYFQGRPVG	25.1	3.5	1.0	3.5	0.3
rB6-3-H5-IGFR	LALLPMLWDYFVATDPQ	35.5	18.1	5.6	3.2	0.3
rB6-4-D8-IGFR	DSILRELRYFARTHIA	36.2	22.5	7.5	3.0	0.3
rB6-4-A8-IGFR	DGVLGQLWQYFAQYPGS	41.1	30.6	10.6	2.9	0.3
rB6-4-H8-IGFR	?PPLDALWEYFTGTARD	38.7	33.0	11.5	2.9	0.3
rB6-3-E2-IGFR	DNVLEGLWSYFALWSQL	20.9	2.2	1.0	2.2	0.5
rB6-3-C2-IGFR	SAVLEYLLAYFARTGAA	31.0	2.1	1.0	2.1	0.5
rB6-4-G8-IGFR	DRALGPLWRYFMVNNQ	38.7	5.5	2.6	2.1	0.5
rB6-3-G5-IGFR	WRILDRLLAYFKESQGD	32.8	2.0	1.0	2.0	0.5
rB6-4-C9-IGFR	DDVLVTLFQYFRASTGV	37.6	30.2	15.1	2.0	0.5
rB6-4-D11-IGFR	FDVLTWLGRYF*MNTGK	36.6	5.5	3.0	1.8	0.5
rB6-4-B11-IGFR	RDVLDGLREYFRASVGG	25.2	4.2	2.4	1.8	0.6
rB6-4-E11-IGFR	IKTLNDLLAYFRGDLDV	38.1	29.8	22.2	1.3	0.7
rB6-3-G3-IGFR	DEALLWLMRYFRGSPSP	31.6	8.7	7.2	1.2	0.8
rB6-4-H12-IGFR	ESPLDALRAYFSGRRNW	40.1	2.8	2.5	1.1	0.9
rB6-4-G12-IGFR	IQSL*DLLQYFVSSPSV	36.7	32.5	31.4	1.0	1.0
rB6-3-C4-IGFR	GGILD?LQDYFRSTDVG	37.1	6.2	13.5	0.5	2.2

Figure 3D (Con't)

**Clone** . . . . .  
**Design** . . . . .  
R20 $\beta$ -4-F8-IR

**Figure 4A**

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
F815-4-H9-IR	HLCVLEELFWGASLFGYCSG	--	--	--	--	--
F815-3-B1-IR	PLCVLEELFWSTPLFGQCSY	34.9	0.9	37.6	<0.1	40.8
F815-3-D1-IR	HLCVLEELFWGASLFAQCVG	31.7	0.9	35.8	<0.1	39.3
F815-3-D4-IR	DLCVLEELFWGASRFGQCSG	30.4	0.9	33.5	<0.1	38.9
F815-3-C5-IR	HLCVLEELFWGASLFGQAG	31.5	0.9	33.6	<0.1	38.8
F815-4-H3-IR	HLCVVEELFWGASLFGQCSG	31.1	0.8	31.2	<0.1	38.5
F815-3-A5-IR	NLCDLELVFWGASLFRQCSG	33.7	1.0	37.2	<0.1	38.4
F815-3-D7-IR	PLCVLEEQFWGASLFGQCSG	37.4	1.1	40.9	<0.1	38.3
F815-3-A1-IR	QLCVLEELFWGASEFQCSG	33.6	0.9	34.3	<0.1	38.3
F815-4-H4-IR	HLCELEELFWGASLFGQCSG	29.8	0.9	34.8	<0.1	38.0
F815-3-A3-IR	PLCVLEELFWGESLFGQCSG	31.1	0.9	32.7	<0.1	38.0
F815-3-B3-IR	HLCVLEELFWGASRFGQCSG	32.8	1.0	39.1	<0.1	37.9
F815-3-A4-IR	KLCVLEELFWGASLFGQCSG	33.7	1.0	37.5	<0.1	37.5
F815-3-D2-IR	YLCVLEELSWGASLFGQCSG	32.5	1.0	36.9	<0.1	37.5
F815-3-C4-IR	HLCVLEELFWGESLFGQCSG	31.9	0.9	34.1	<0.1	37.4
F815-3-B4-IR	QLCVLEQFWGESLFGQCSG	31.6	0.8	31.8	<0.1	37.4
F815-3-C1-IR	HLCVLEELFWGGLFSQCSG	33.8	1.0	36.7	<0.1	37.3
F815-4-G9-IR	HLCVLEELFWGASLYGQCSG	29.0	0.9	35.0	<0.1	37.3
F815-4-G6-IR	SLCALEEQFWGAALFGYCSG	36.5	1.0	38.9	<0.1	37.1
F815-3-A8-IR	HLCVLEEQFWGASLFDGCAG	34.9	1.0	36.4	<0.1	37.0
F815-4-G5-IR	QLCVLEELFWGASLFGQCSG	34.7	1.1	39.3	<0.1	36.9
F815-3-B5-IR	PLCVLEELFWGAALFGQCSG	26.5	1.0	35.1	<0.1	36.8
F815-4-F4-IR	HLCVLEELFWGASLFGQCTG	33.2	0.9	34.1	<0.1	36.8
F815-3-A2-IR	PLCVLEELFWGGLFGQCSG	28.6	0.8	30.0	<0.1	36.7
F815-3-B6-IR	QLCVLEELVWGASLFGQCSG	32.5	1.0	36.6	<0.1	36.6
F815-4-H7-IR	HLCVVEELVWGASLFGQCSR	31.6	0.9	32.9	<0.1	36.5
F815-4-H8-IR	DLCVLEELFWGASLFGQAG	33.7	1.0	37.6	<0.1	36.4
F815-4-G7-IR	QLCVLEERFWGASLFGQCSG	35.8	1.0	37.0	<0.1	36.4
	NLCVLEELFWGAALFGQCSG	33.7	1.0	35.8	<0.1	36.3

Figure 4B



Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	HLCVLEELFWGASLFGYCSG	--	--	--	--	--
F815-4-F11-IR	RLCVLEERFWGAALFGQCSG	31.8	1.0	33.7	<0.1	34.2
F815-3-A9-IR	PLCVLEELFWGASLFGQCSG	31.9	1.0	35.5	<0.1	34.1
F815-4-G11-IR	SLCVLEELFWGGSRFQCSG	32.3	1.0	34.4	<0.1	33.9
F815-3-D8-IR	HCLLEEQFWGASLFGYCFE	32.3	1.0	33.3	<0.1	33.7
F815-4-G4-IR	HLCVLEEQFWGASLFGQCSG	23.8	1.0	32.2	<0.1	33.7
F815-3-C8-IR	DLCLLEELLWGASRFQCSG	33.9	1.0	35.1	<0.1	33.6
F815-4-G12-IR	YLCVLEERFWGASLFGQCSG	31.7	1.0	33.5	<0.1	33.5
F815-3-D12-IR	HLCVLEEQFWGASLFGSCSG	33.3	1.0	34.8	<0.1	33.4
F815-4-F7-IR	QLCVLEEQFWGASLFGQCSG	33.3	1.0	34.3	<0.1	33.4
F815-4-F2-IR	HLCVLEELF*GESLFGYCSG	26.1	1.0	33.8	<0.1	33.3
F815-3-B9-IR	HLCVLEELFWGASLFGQCSG	33.6	1.1	35.7	<0.1	33.2
F815-4-H2-IR	PLCVLEELFWGASHFGQCSG	36.1	1.2	38.4	<0.1	33.0
F815-4-E11-IR	HLCVLEELVWGASLFGQCAG	33.2	1.1	35.4	<0.1	33.0
F815-3-A11-IR	QLCVLEELIWGASLFGQCAG	27.9	1.0	31.5	<0.1	32.8
F815-4-F6-IR	HLCGLEELFWGASLFGQCSG	37.7	1.2	40.1	<0.1	32.7
F815-3-D9-IR	HLCVLEELVWGESLFGQCSG	32.3	1.1	34.6	<0.1	32.6
F815-3-C11-IR	RLCVLEELVWGASLFGQCSG	31.4	1.0	32.5	<0.1	32.5
F815-4-G2-IR	RLCILEELFWGASLFGQCSG	33.4	1.1	35.7	<0.1	31.9
F815-3-C9-IR	HLCVLEELFWGATLFDQCSG	30.2	1.1	34.3	<0.1	31.4
F815-4-H10-IR	HLCFLEELFWGASLFGQCSG	29.7	1.0	31.4	<0.1	31.0
F815-4-F3-IR	HLCVLEELFWAAPLFGQCSG	31.9	0.9	27.6	<0.1	29.4
F815-4-F5-IR	HLCVLEELVWGASLFAQCSA	19.4	1.0	28.0	<0.1	28.9
F815-4-H1-IR	NLCVLEELFWGASLFGQCPG	12.3	0.9	24.8	<0.1	26.8
F815-4-E5-IR	RLCVLEELFWGASLFGQCSG	6.9	1.0	15.8	0.1	16.5
F815-4-H5-IR	PLCVLEELFWGASLFGQCPG	3.5	1.0	13.6	0.1	14.0
	NLCVLEELFWGASLFGQCSG	5.5	1.0	13.1	0.1	13.5
F815-3-C10-IR	QLCVLG#RFWGGSLCGYCSG	3.5	1.1	5.2	0.2	4.5

Figure 4B (Con't)

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons		
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
F815-4-F11-IGFR	HLCVLEELFWGASLFGYCSC	39.1	1.8	27.7	0.1	15.4		
F815-4-E12-IGFR	PLCFLQELFGGASLGGYCSC	33.4	12.3	1.0	12.3	0.1		
F815-4-H10-IGFR	FMCGLQELVGGAAALLGHCSG	33.7	15.1	1.7	8.9	0.1		
F815-4-B7-IGFR	PLCFLQELFGGSLSGYCSC	30.1	8.5	1.0	8.5	0.1		
F815-3-B5-IGFR	FLCGLEELAWGVSRSYCFG	35.2	23.9	4.8	5.0	0.2		
F815-4-D12-IGFR	PLCFLAELFSGSALGGDCSR	33.9	4.8	1.0	4.8	0.2		
F815-4-C11-IGFR	PLCVLQELFGGSLGGYCSC	33.6	7.0	1.8	3.9	0.3		
F815-4-C7-IGFR	QLCVLE#LFWGACLFGYCAG	13.9	4.6	1.8	2.6	0.4		
F815-4-E7-IGFR	FLCVLQELSGVASLFGQCSG	16.8	2.0	1.0	2.0	0.5		
F815-4-G7-IGFR	RVCVLEQLVWGASLFGA*SG	26.9	3.8	1.9	2.0	0.5		
F815-4-A10-IGFR	FYCGLEELSWGAAALFGYCSC	30.4	9.0	5.0	1.8	0.6		
F815-3-B3-IGFR	FLCVLGLFWDASLFGQCSG	30.8	3.7	2.2	1.7	0.6		
F815-3-G1-IGFR	HLCVLAALFWCATLLGGCAG	7.6	1.0	2.0	0.5	2.0		
F815-4-G12-IGFR	QRCIRAAALFWCATLLGGCAG	20.5	1.0	2.0	0.5	2.0		
F815-3-H1-IGFR	HQCIPDGMSQGAALRGNCSD	7.6	1.0	2.5	0.4	2.5		
	HLCVLEDELWGVSLFGYCSC	18.4	1.0	6.8	0.1	6.8		

Figure 4C

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
F820-4-B5-IR		<u>HLCVLEELFWGASLFGYCSCG</u>	39.1	1.8	27.7	0.1	15.4
F820-4-B5-IR		HLCVLEELFWGASLFGYCSCG	28.1	0.9	17.9	<0.1	21.1
F820-4-A2-IR		TCAFWKNGSGVRRCSVTAVV	34.0	1.6	22.7	0.1	13.9
F820-4-E2-IR		PLCGLKN.SGVRLCSSPALV	21.3	0.7	9.0	0.1	13.4
F820-4-D10-IR		PLCLQEELFWGASLFGYCSCG	34.1	1.0	12.1	0.1	12.1
F820-4-H7-IR		PLCDLEELFWGASLFGDCPG	14.2	0.6	6.5	0.1	11.6
F820-4-G6-IR		DLCVLEELFWGASLFGSCSG	14.0	0.5	6.1	0.1	11.5
F820-4-C2-IR		PLCVLEELFWGASLFGSCSG	38.1	1.2	11.8	0.1	9.9
F820-4-B4-IR		PLCLVEELFWGASLFGSCSG	15.1	0.7	6.4	0.1	8.7
F820-4-C7-IR		PLCDLEELFWGASLFGSCSG	46.3	2.7	22.2	0.1	8.2
F820-4-F10-IR		GLCFLEELFWGASLFGSCSG	14.5	0.6	4.7	0.1	8.0
F820-4-G5-IR		PLCVVEELFWGASLFGSCSG	8.8	0.6	4.4	0.1	7.5
F820-4-F2-IR		RLCVLEELFWGASLFGSCSG	11.7	0.6	4.2	0.1	7.4
F820-4-H8-IR		PLCVLEELFWGASLFGSCSG	16.0	0.6	4.7	0.1	7.3
F820-4-D7-IR		NLCVVEELFWGASLFGSCSG	14.5	0.8	5.9	0.1	7.1
F820-4-B2-IR		QLCVLEELFWGASLFGSCSG	5.0	0.4	2.4	0.2	6.9
F820-4-C3-IR		HLCVLEELFWGASLFGSCSG	37.5	1.1	7.5	0.2	6.6
F820-4-H4-IR		PLCVLEELFWGASLFGSCSG	21.2	1.1	6.4	0.2	5.9
F820-4-B10-IR		PLCVLEELFWGLSLDKNCS	7.5	0.7	3.7	0.2	5.6
F820-4-A5-IR		QLCVLEELFWGASLFGSCSG	5.3	0.8	4.4	0.2	5.2
F820-4-F6-IR		PLCDLEALFWGESLFGSCSG	5.7	0.6	3.0	0.2	4.9
F820-4-F1-IR		HLCVLEELFWGASLFGSCSG	9.1	1.0	4.7	0.2	4.7
F820-4-A3-IR		DLCVLEELFWGASLFGSCSG	5.9	0.8	3.5	0.2	4.5
F820-4-D1-IR		DLCVLEELFWGASLFGSCSG	25.7	2.3	10.5	0.2	4.5
F820-4-F5-IR		QLCVLEELFWGASLFGSCSG	3.7	0.6	2.7	0.2	4.2
F820-4-F12-IR		HLCVLEELFWGASLFGSCSG	11.3	0.6	2.2	0.3	3.5
F820-4-A11-IR		HLCVLEELFWGASLFGSCSG	7.6	0.8	2.7	0.3	3.5
F820-4-E8-IR		PLCVLEELFWGASLFGSCSG	8.0	1.2	4.3	0.3	3.5
F820-4-H3-IR		HLCVLEELFWGASLFGSCSG	17.5	2.6	9.0	0.3	3.4

Figure 4D



Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		<u>HLCVLEELFWGASLFGYCSG</u>	--	--	--	--	--
	F820-4-A8-IR	QLCVMEELFWGASRFGQCSG	6.4	0.7	2.4	0.3	3.4
	F820-4-G1-IR	HLCVLEELFWGASMFQCSG	3.9	0.6	1.9	0.3	3.4
	F820-4-F3-IR	QLCVLEEMFWGSRFVQCSA	9.8	1.3	3.6	0.4	2.9
	F820-4-D6-IR	PLCILEELFWGEALFDQCGA	5.4	1.2	3.2	0.4	2.6
	F820-4-A1-IR	YLCVQEELFWGASLFGYCSV	25.5	2.4	6.1	0.4	2.5
	F820-4-H2-IR	HLCALAEAFPGSLFNSCQG	15.9	1.6	4.1	0.4	2.5
	F820-4-F4-IR	HLCVLEERFWGASLFGQCSG	6.8	1.9	4.7	0.4	2.5
	F820-4-B6-IR	QLCDLEELFWGASLFGYCPG	4.1	0.8	1.9	0.4	2.4
	F820-4-B11-IR	HLCVLEERFWGASLFGQCSG	22.2	3.1	7.0	0.4	2.3
	F820-4-H6-IR	QLCVLEELFWGASLFGQCSG	4.1	1.1	2.4	0.5	2.2
	F820-4-H9-IR	PLCVLEELFWGAAQFGQCSG	3.1	0.9	1.9	0.5	2.1
	F820-4-D3-IR	QLCDLEERFWGVSFLFGLCSG	4.6	1.3	2.5	0.5	1.9
	F820-4-C1-IR	QLCVLEEVFWGASLFGGLCTG	13.0	1.1	2.1	0.5	1.9
	F820-4-D12-IR	QL.DLNTWSGLCLCSVTVRV	10.4	1.2	2.0	0.6	1.7
	F820-4-B8-IR	DLCVLEESLWGKALFGYCSD	7.2	2.2	3.4	0.6	1.5
	F820-4-C6-IR	HLCVLEEVFWGSSMFGDCSG	13.9	2.5	2.8	0.9	1.1
	F820-4-C10-IR	HLCDLEELFWGASLFGDCQG	5.3	2.6	2.9	0.9	1.1
	F820-4-D4-IR	QLCVLDALMWGCRLLGHQCG	3.5	2.3	2.1	1.1	0.9
	F820-4-E1-IR	QLCVLEEKFWGTSLFGDCMG	1.6	1.6	1.5	1.1	0.9
	F820-4-B3-IR	HLCVLEEVFWGAAQFGSCSG	15.9	0.6	5.0	1.2	0.8
	F820-4-D2-IR	QLCVLEELFWGSPMFGYCSG	7.8	3.2	2.5	1.3	0.8
	F820-4-C5-IR	HLCDLEELFWGASGFAQCYG	21.5	4.0	2.3	1.8	0.6

Figure 4D (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
A6L-3-C4-IR	HLCVLEELFWGASLFGYCSCG	--	--	--	--	--
A6L-3-D7-IR	DLCVLEERFWGASLFGQCSCG	36.9	1.0	40.5	<0.1	42.5
A6L-3-A1-IR	QLCVLEELHWGASLFGYCSCG	38.6	1.0	40.1	<0.1	40.7
A6L-3-C1-IR	PLCVLEEQFWGASLFGQCSCG	39.6	1.1	44.8	<0.1	40.6
A6L-3-D5-IR	YLCDLEERFWGASLFGQCSCG	37.3	1.0	40.3	<0.1	40.3
A6L-3-A4-IR	HLCVLEELFWGASLFGQCSCG	42.9	1.1	44.4	<0.1	40.2
A6L-3-D3-IR	HLCVLEELFWGASLFGQCSCG	26.7	1.1	42.2	<0.1	40.2
A6L-3-B1-IR	HLCVLEERFWGASLFGQCSCG	34.6	0.9	36.9	<0.1	39.8
A6L-3-B5-IR	HLCVMEELFWGASLFGQCSCG	33.9	1.0	38.7	<0.1	39.3
A6L-3-B2-IR	HLCVLEERFWGASLFGQCSCG	35.3	1.1	42.4	<0.1	38.6
B6H-4-G12-IR	HLCVLEERFWGASLFGQCSCG	38.1	1.1	42.7	<0.1	37.7
B6C-4-H10-IR	HLCVLEELFWGASLFGQCSCG	31.6	1.1	39.6	<0.1	36.7
B6H-4-G8-IR	QLCVLEELFWGASLFGQCSCG	38.5	1.1	41.1	<0.1	36.5
A6L-3-D6-IR	HLCVLEEMFWGASLFGQCSCG	31.7	1.1	39.7	<0.1	36.2
B6C-4-H3-IR	HLCVLEELFWGASLFGQCSCG	35.5	1.0	37.2	<0.1	36.1
B6C-4-F1-IR	QLCVLEELFWGASLFGQCSCG	32.9	1.1	38.7	<0.1	35.8
B6H-4-E8-IR	QLCVLEELFWGASLFGQCSCG	37.4	1.2	40.5	<0.1	34.8
B6C-4-G1-IR	QLCVLEELFWGASLFGQCSCG	30.2	1.0	35.7	<0.1	34.3
B6H-4-E9-IR	HLCVLEEFWDGSLFGQCSCG	34.9	1.2	40.2	<0.1	33.7
B6C-4-F5-IR	HLCVLEERFWGASLFGQCSCG	34.4	1.2	38.8	<0.1	33.2
B6C-4-F11-IR	QLCVLEELFWGASLFGQCSCG	34.7	1.2	39.6	<0.1	32.8
B6C-4-E6-IR	HLCVLEELFWGASLFGQCSCG	34.0	1.2	37.2	<0.1	31.7
B6C-4-E12-IR	HLCVLEELFWGASLFGQCSCG	32.3	1.2	37.4	<0.1	30.6
B6C-4-G10-IR	HLCVLEELFWGASLFGQCSCG	30.9	1.1	33.3	<0.1	30.2
B6C-4-F8-IR	HLCVLEELFWGASLFGQCSCG	33.0	1.3	40.3	<0.1	30.1
20C-3-B5-IR	QLCVLEEQFWGASLFGQCSCG	36.4	1.4	39.8	<0.1	29.3
B6C-4-G3-IR	HLCVLEERFWGASLFGQCSCG	26.6	1.1	32.5	<0.1	29.2
20C-3-B7-IR	HLCVLEELFWGASLFGQCSCG	34.0	1.4	38.8	<0.1	28.3
	PLCVLEELVWGASLFGQCSCG	29.5	1.2	32.9	<0.1	28.3

Figure 4E

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20C-3-B4-IR	HLCVLEELFWGASLFGYCSCG	28.9	1.1	31.1	<0.1	28.0
20C-3-C11-IR	NLCVLEELFWGESLFGQCSG	30.2	1.1	31.0	<0.1	27.7
B6C-4-G2-IR	HLCVLEEQFWGGSFLFGYCSR	29.4	1.3	35.3	<0.1	27.5
20C-3-B8-IR	HLCFLEEVFWGAALFAQCSG	28.5	1.1	31.2	<0.1	27.4
20C-3-C10-IR	HLCDLEVLFWGSALFGQCSG	32.1	1.2	33.6	<0.1	27.1
20C-3-B6-IR	HLCVMEELFWGASLFGQCSG	29.7	1.2	31.9	<0.1	26.7
A6L-3-A3-IR	HLCVLEERFWGASLFWQCSG	14.4	1.1	28.3	<0.1	26.5
A6L-3-B3-IR	HLCVLEEQYWGESLFGYCSCG	38.7	1.7	43.4	<0.1	26.3
20C-3-A5-IR	PLCVLEEQFWGASLFAYCSC	22.9	1.1	27.6	<0.1	26.0
20C-3-B11-IR	QLCVLEELFWGESLFAQCLG	30.0	1.3	32.7	<0.1	25.8
20C-3-B3-IR	HLCVLEELFWQSLFGHCSD	29.3	1.2	31.2	<0.1	25.7
20C-3-C12-IR	HLCVLEELVWGASLFGFCSCG	29.6	1.3	31.8	<0.1	24.8
20C-3-C3-IR	LLCVLEEQFWGASLFGQCSG	30.1	1.2	30.1	<0.1	24.3
20C-3-C2-IR	RLCVLEELFWGESLFGQCSG	29.9	1.3	29.8	<0.1	23.8
20C-3-A11-IR	ELCFLEELFWGASLFGQCSG	25.9	1.2	27.4	<0.1	23.0
20C-3-A4-IR	HLCVLEELFWGASLYGQCS	27.2	1.2	27.5	<0.1	22.9
20C-3-A6-IR	HLCVLEELFWGASLFAQCPG	26.1	1.2	27.5	<0.1	22.8
B6C-4-E4-IR	NLCVLEELFWGASEFFGQCSG	34.5	1.7	39.1	<0.1	22.7
20C-3-A9-IR	DLCVLEEQWGSALFRYCSCG	29.7	1.3	29.3	<0.1	22.7
B6C-3-C5-IR	HLCVLEEQFWGVALFGNCSCG	33.5	1.7	37.7	<0.1	22.5
20C-3-B1-IR	HLCVLEEQWGSALFGQCSG	30.2	1.2	26.7	<0.1	22.0
20C-3-A10-IR	HLCVLEEQWGSALFGQCSG	29.0	1.3	28.5	<0.1	21.5
20C-4-F1-IR	HLCVLEERFWGGALFGQCTA	29.1	1.4	29.5	<0.1	20.7
20C-4-E1-IR	QLCVLEELFWGTSLFAGCSG	28.3	1.4	29.7	<0.1	20.6
20C-3-B12-IR	QLCVLEELFWGASLFGYCSCA	27.0	1.3	25.8	<0.1	20.2
20C-3-A8-IR	HLCVLEELFWGASLFGQCS	21.1	1.1	21.2	0.1	20.0
20C-3-A7-IR	FLCVLEELYWGASQFGQCSG	21.9	1.3	23.0	0.1	18.3
B6C-4-E10-IR	HLCVLEEQFWGASLFGYCSCG	35.2	2.2	38.0	0.1	17.5

Figure 4E (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGF/IR	IR/IGFR
20C-3-A1-IR	HLCVLEELFWGASLFGYCSCG	21.0	1.1	17.6	0.1
20C-3-C1-IR	RLCALEELFWGASLFGQCSG	30.6	1.4	21.9	0.1
A6L-3-D2-IR	HLCVLEELFWGAALFHQCSG	7.0	1.1	14.9	0.1
B6C-4-G12-IR	RLCVLEELFWGASLFGQCSG	31.1	2.5	33.5	0.1
B6H-4-F9-IR	QLCVLEELFWGASLFGQCSG	39.3	3.6	43.1	0.1
B6C-4-E3-IR	QLCLLEELFWGASLFGQCSG	34.6	5.3	40.0	0.1
20C-3-B10-IR	HLCVLEELFWGTSLFGQCSG	29.9	16.9	31.7	0.5
20C-3-A3-IR	RLCVLEELVWGASLFDQCSR	28.4	19.1	25.3	0.8

Figure 4E (Con't)

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		<u>HLCVLEELFWGASLFGYC</u> SG	39.1	1.8	27.7	0.1	15.4
F815-4-D10-IGFR		PLQALCEKFFGAWMFGYC	31.2	13.9	1.0	13.9	0.1
F815-4-H11-IGFR		HLQVLCELFGGVYLFGYCSG	27.2	19.2	1.7	11.3	0.1
F815-4-C8-IGFR		PLFDLCELFGGASLSGYCYG	35.4	17.4	1.6	10.9	0.1
F815-4-E8-IGFR		HL*ALCELFGGVWSFGYCVG	29.5	16.9	1.7	9.9	0.1
F815-4-E11-IGFR		QLGVLCMFGGAFRLGYCQG	36.6	25.7	2.7	9.5	0.1
F815-4-A7-IGFR		HLQDLCELFGGAYLFGYC	29.6	16.0	3.8	4.2	0.2
F815-3-D3-IGFR		QLQVLCELFGGAVSLRLLW	33.7	3.5	1.0	3.5	0.3
F815-4-F7-IGFR		PLGVLCCEQFGGAFRFGYC	33.6	18.9	9.9	1.9	0.5
F815-4-A9-IGFR		PL*GLCELFGGASLFGYC	7.5	1.7	2.3	0.7	1.4
F815-4-B12-IGFR		DLRVLCLELFGGAYVLGYCSE	35.1	3.7	12.6	0.3	3.4

Figure 5

03052300"020003000300

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
R20 $\alpha$ -3-20A4-IR	XXXXXXXXXXXXXXXXXXXX EIEAEWGRVRCLVYGRGVGG	--	--	--	--
R20 $\beta$ -4-A7-IR	EIEAEWGRVRCLVYGRGVGG	50.2	1.6	23.1	0.1
R20 $\beta$ -4-D8-IR	WLDQEWAVQCEVYGRGCPS	44.2	1.3	24.0	0.1
		44.8	1.4	24.2	0.1
					17.3

Figure 6A

Clone Parental/Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
D815-4-A8-IR	WLDQEWAWVQCEVYGRGCP	44.8	1.4	24.2	<0.1	17.3
D815-4-A8-IR	WLDLEWAQVQCEVYGRGCP	48.0	1.0	48.4	<0.1	48.4
D815-4-D10-IR	WLDQEWAWVQCEVYGRGCP	49.2	1.0	48.2	<0.1	48.2
D815-4-D9-IR	WLDQEWQVQVQVYGRGCT	47.5	1.0	48.0	<0.1	48.0
D815-4-A11-IR	RLDEEWARVQCEVYGRGCR	47.9	1.0	48.0	<0.1	48.0
D815-4-E12-IR	WLEQEWAWIQCEVYGRGCP	49.0	1.0	47.6	<0.1	47.6
D815-4-B7-IR	WLEQEWAWVQCEVYGRGCP	45.4	1.0	47.2	<0.1	47.2
D815-4-D11-IR	WLDDEEWIQCCKVYGRGCP	49.5	1.0	47.0	<0.1	47.0
D815-4-D12-IR	WLEQEWAWVQCEVYGRGCP	48.1	1.0	46.6	<0.1	46.6
D815-4-F8-IR	WLDQEWAWIQCEVYGRGCP	47.8	1.0	46.4	<0.1	46.4
D815-4-A9-IR	SLDWAWWLQCEVYGRGCP	47.7	1.0	45.8	<0.1	45.8
D815-4-E9-IR	WLEQEWQVRLVYGRGCP	47.8	1.0	45.8	<0.1	45.8
D815-4-B10-IR	WLDQEWAWVQCEVYGRGCP	49.0	1.0	45.6	<0.1	45.6
D815-4-H8-IR	WLDQEWAGVLCEVYGRGCP	49.0	1.0	45.6	<0.1	45.6
D815-4-E10-IR	SLDKEWVLCVYGRGCP	47.0	1.0	45.6	<0.1	45.6
D815-4-D7-IR	WLEQEWAWVQCEVYGRGCR	44.5	1.0	45.4	<0.1	45.4
D815-4-G9-IR	WLEEWAWVQCAVYGRGCS	44.2	1.0	44.2	<0.1	44.2
D815-4-G12-IR	WLDQEWALVQCEVYGRGCP	44.3	1.0	43.7	<0.1	43.7
D815-4-E11-IR	WLDQEWAWVQCEVYGRGCP	45.5	1.0	43.0	<0.1	43.0
D815-4-H7-IR	WLEQEWAWVQCEVYGRGAS	46.2	1.0	43.0	<0.1	43.0
D815-4-F12-IR	WLDQEWAWVECEVYGRGCP	47.2	1.0	42.6	<0.1	42.6
D815-4-E8-IR	WLDQEWAWVEQVYGRGCP	47.9	1.0	42.6	<0.1	42.6
D815-4-F9-IR	QLDQEWAWVLCVYGRGCP	46.4	1.0	41.8	<0.1	41.8
D815-4-A10-IR	WLDHE*AWVQCEVYGRGCP	47.3	1.0	41.2	<0.1	41.2
D815-4-C7-IR	QLEQEWAWVRCEVYGRGCS	37.7	1.0	40.0	<0.1	40.0
D815-4-H10-IR	WLDQEWAWVQVYGRGCLS	47.0	1.0	39.8	<0.1	39.8
D815-4-C9-IR	WLDQEWAWVRCEVYGLGCP	44.2	1.0	39.8	<0.1	39.8
D815-4-F11-IR	WLDQEWAWMKCELYGRGCP	40.4	1.0	39.2	<0.1	39.2
D815-4-H12-IR	WLEQEWAWVQCEVYGRGCLS	45.4	1.0	38.6	<0.1	38.6
D815-4-A7-IR	SLDQEWAWVQCEVYGRGCLS	37.3	1.0	37.3	<0.1	37.3
D815-4-H11-IR	WLDHEWAWVQCEVYGRGCT	2.4	1.0	37.2	<0.1	37.2
D815-4-F7-IR	WLDVEWAWVQCEVYGRGCP	32.4	1.0	34.7	<0.1	34.7

Figure 6B

# Figure 6B (Con't)

Clone Parental/Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR IR/IGFR
D815-4-G8-IR	WLDQEWAWVQCEVYGRGCP	--	--	--	--
D815-4-G7-IR	QLDQEWARVRCEVWGRGCSS	27.8	1.0	33.6	<0.1 33.6
D815-4-G11-IR	WLDLEWAQVQCKVYGRGCP	34.7	1.0	32.3	<0.1 32.3
D815-4-E7-IR	WLDEEAWVQCVYGRGCP	30.7	1.0	28.6	<0.1 28.6
D815-4-A12-IR	WLDQEWAWVQCEVWGRGCAF	33.0	1.0	26.4	<0.1 26.4
D815-4-B11-IR	WLDREWAQVQCEVYGRGCLS	28.4	1.0	19.0	0.1 19.0
D815-4-D8-IR	WLDAEWEVQCEVYGRGCRP	22.1	1.0	18.8	0.1 18.8
	SLDREWAYVQCQVYGRGCSS	20.8	1.0	14.6	0.1 14.6

Figure 6B (Con't)



Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Parental/Design	<u>WLDQEWAWVQCEVYGRGCP</u> S	44.8	1.4	24.2	0.1	17.2
D820-3-H2-IR	RLDLEWANIQCEVYGRGCPS	23.9	1.0	40.0	<0.1	40.0
D820-3-C4-IR	WLEQEWARVQCEVYGRGCSS	31.0	1.0	39.5	<0.1	39.5
D820-3-C3-IR	WLEQEWILVECEVYGRGCPT	35.2	1.0	39.4	<0.1	39.4
D820-3-G6-IR	WLEQEWAQVQCEVWGRGCPS	33.8	1.0	38.8	<0.1	38.8
D820-3-D2-IR	WLDQEWEWIQCEVYGRGCPL	35.6	1.0	37.8	<0.1	37.8
D820-3-D3-IR	LLDEEWAQIECEIYGRGCPS	34.8	1.0	37.7	<0.1	37.7
D820-3-B5-IR	ALEEEWAWVQCEVYGRGCHF	34.1	1.0	37.1	<0.1	37.1
D820-3-E2-IR	C?EQEWGLVQCEVYGRGCPS	34.4	1.0	37.0	<0.1	37.0
D820-3-B3-IR	WLEQEWAYVQCEVYGRGCPS	33.6	1.0	36.7	<0.1	36.7
D820-3-B6-IR	WLEHEWAQVQCEVWGRGCPY	31.2	1.0	36.6	<0.1	36.6
D820-3-D4-IR	WLEQEWAEVRCEVYGRGCPR	32.0	1.0	36.2	<0.1	36.2
D820-3-C2-IR	?LEQEWAWVQCEVYGRGCPS	33.7	1.0	35.6	<0.1	35.6
D820-3-F6-IR	WLEQEWAGIQCKVYGRGCPS	30.8	1.0	35.2	<0.1	35.2
D820-3-D5-IR	RLEQEWAQVQCEVWGRGCLP	30.5	1.0	34.8	<0.1	34.8
D820-3-F5-IR	QLDHEWAGIQCEVWGRGCPS	29.8	1.0	34.6	<0.1	34.6
D820-3-H3-IR	WLEQEWAAIQCEVYGAGCRS	30.2	1.0	33.8	<0.1	33.8
D820-3-G2-IR	SLEQEWAWVQCVVYGRGCPI	31.3	1.0	33.0	<0.1	33.0
D820-3-H6-IR	WLEQEWDDQVLCEVYGRGCPY	30.3	1.0	32.2	<0.1	32.2
D820-3-F3-IR	WLEQEWAAQV?CEVYGRGCA?	28.6	1.0	30.7	<0.1	30.7
D820-3-B4-IR	WMDQEWAWVQCEVYGRGCPS	33.1	1.0	30.5	<0.1	30.5
D820-3-C5-IR	QLDQEWAWIQCEVYGRNCRT	29.1	1.0	30.3	<0.1	30.3
D820-3-F4-IR	TLEQEWAAQVICEVYGRGCLS	25.9	1.0	29.5	<0.1	29.5
D820-3-H5-IR	RLEQEWAAQVQCEVWGRGCLS	26.3	1.0	28.6	<0.1	28.6
D820-3-A6-IR	WLDQEWALVQCEVYGRGCPA	24.8	1.0	26.0	<0.1	26.0
D820-3-A2-IR	WLDQEWAAQIQCHVWGRGCPA	23.7	1.0	25.6	<0.1	25.6
D820-3-G5-IR	WLEQEWAWVQCEVYGRGCPS	22.6	1.0	25.0	<0.1	25.0
D820-3-G3-IR	RLEEEWAWVQCQVYGRGCPS	22.2	1.0	23.9	<0.1	23.9
D820-3-E3-IR	WLEQEWVRIQCEVYGRGCPS	20.6	1.0	22.7	<0.1	22.7



Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		<b>WLDQEWAWVQCEVYGRGCPS</b>	<b>44.8</b>	<b>1.4</b>	<b>24.2</b>	<b>0.1</b>	<b>17.2</b>
D820-3-E5-IR		WLEQEWTVQCEVYGGCPS	25.9	1.0	22.6	<0.1	22.6
D820-3-D1-IR		WLEKEWAGVQCEIYGRGCPS	27.3	1.0	22.4	<0.1	22.4
D820-3-E1-IR		WLEEEWAWRCEVYGRGCQS	22.4	1.0	21.9	<0.1	21.9
D820-3-F1-IR		WLEHEWAQIQCELYGRGCTY	22.0	1.0	21.0	<0.1	21.0
D820-3-B2-IR		ALEEEWAWVQCEVYGRGCPS	13.1	1.0	18.4	0.1	18.4
D820-3-A3-IR		WLEQEWAGVQCEVYGRGCPS	23.5	1.0	18.4	0.1	18.4
D820-3-H4-IR		WLDDEWAQIQCEIYGRGCQS	25.6	1.0	17.5	0.1	17.5
D820-3-G1-IR		QLEEEWAGVQCEVYGRECPs	14.5	1.0	16.3	0.1	16.3
D820-3-C1-IR		WLEQEWLLVQCGVYGRGCPS	27.8	1.0	13.9	0.1	13.9
D820-3-A1-IR		WLDQEWAWIQCEVYGRGCRS	14.7	1.0	12.8	0.1	12.8
D820-3-A5-IR		WLEQEWAGVQCEVSGRGCPs	6.4	1.0	6.3	0.2	6.3
D820-3-H1-IR		W7DQEWALIQCEVYGRGCPS	13.7	1.0	6.2	0.2	6.2
D820-3-A4-IR		SLDEEWAGVLCEVYGRGCPF	6.0	1.0	4.3	0.2	4.3
D820-4-E12-IR		SVDQELEWLMCHFQGRVCPs	34.9	9.0	10.9	0.8	1.2
D820-4-B12-IR		WLEQERAWIWCIEIQGSGCRA	32.2	8.6	1.0	8.6	0.1



Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
D820-3-D5-IGFR		WLDQEWAWVQCEVYGRGCPS	44.8	1.4	24.2	0.1	17.3
D820-3-E4-IGFR		WVNQALGGVQSDVQRRQCS	29.6	3.8	1.0	3.8	0.3
D820-3-C5-IGFR		LLDHEWPWVGCEVCGRGSLS	27.1	3.2	1.0	3.2	0.3
D820-3-F4-IGFR		WLHQELAWVRGEGYPRGRRS	25.0	3.1	1.0	3.1	0.3
D820-3-F6-IGFR		WLGHDWANIQCEVYGLGCPC	3.9	2.7	1.0	2.7	0.4
D820-3-G4-IGFR		WIDQEGVRVQCEA*GRAFPS	26.7	2.6	1.0	2.6	0.4
D820-3-E2-IGFR		WRDEEWAWVQGVQGRGWA	3.8	2.6	1.0	2.6	0.4
D820-3-G6-IGFR		RLGVESWFRKVVYGRDSTS	15.3	2.6	1.0	2.6	0.4
D820-4-E11-IGFR		WLAQGWAGVQCIVYGRGCRN	20.3	2.4	1.0	2.4	0.4
D820-4-H11-IGFR		WLEEE*AGIQCV?GRGCPS	12.6	1.0	3.0	0.3	3.0
D820-4-D11-IGFR		WLDQEWVQVRCVYGRGCPS	8.1	1.0	4.6	0.2	4.6
D820-4-A8-IGFR		WLEEEWAQVQCIVYGRGCAS	4.5	1.0	5.3	0.2	5.3
D820-4-F9-IGFR		WLDLE*EWLQCEVYGRGCAT	3.2	1.0	5.5	0.2	5.5
D820-4-C8-IGFR		WLEEEWAQVQCEVYGRGCPS	9.4	1.0	5.8	0.2	5.8
D820-4-D7-IGFR		WLDQEWARVQCEVWGRGCTY	11.6	1.0	5.9	0.2	5.9
D820-4-E10-IGFR		WLDVE*AWVQCEVWGRGCPS	10.1	1.0	8.9	0.1	8.9
D820-4-E7-IGFR		WLEEEWAQVQCEVYGLGCQS	34.1	3.5	33.4	0.1	9.5
D820-4-H8-IGFR		WLDQEWAWVQCEVYGRGCPS	18.4	1.0	10.1	0.1	10.1
D820-4-A11-IGFR		?LEHEWAQIQCEV?GRGCQS	26.7	2.6	27.0	0.1	10.4
D820-4-C9-IGFR		WLDQEWAWVQCEVYGRGCPS	31.9	3.0	32.2	0.1	10.7
D820-4-E9-IGFR		WLDQEWAWVQCEVYGRGCPS	16.1	1.0	11.7	0.1	11.7
D820-4-B10-IGFR		WLDQEWAWVQCEVYGRGCPS	8.0	1.0	12.5	0.1	12.5
D820-4-F10-IGFR		?LEHEWAQIQCEV?GRGCQS	19.6	1.0	14.9	0.1	14.9
D820-4-B9-IGFR		WLDQEWAWVQCEVYGRGCPS	19.3	1.0	17.3	0.1	17.3
D820-4-G8-IGFR		WLDQEWAWVQCEVYGRGCPS	19.3	1.0	21.5	<0.1	21.5
		GLEQGCPCWVGLVQCRGCPS	27.8	1.0	25.7	<0.1	25.7
		WLEEEWAQVQCEVYGRGCPS	31.7	1.0	26.5	<0.1	26.5
		WLDQEWAWVQCEVYGRGCPS	25.6	1.0	29.3	<0.1	29.3

Figure 6D





### Figure 6E

	Sequence	HIR affinity mol/l
J228	HPPLEHLKAFLN-NH <sub>2</sub>	2.4*10 <sup>-5</sup>
J229	APTFYAWFNQQT-NH <sub>2</sub>	2.4*10 <sup>-6</sup>
S122	HPSTKEIYAKLLK	9.3*10 <sup>-6</sup>
S123	HPSTNQMLMKLFK	1.6*10 <sup>-5</sup>
S124	HPPLSELKLFLIKK	2.3*10 <sup>-5</sup>

**Figure 7**

J-nr	Sequence	HIR affinity mol/l
J101	ACVWPTYWNCG	$5.0 \cdot 10^{-6}$
J103	Ac-CVWPTYWNCG	$3.0 \cdot 10^{-5}$
J104	Bz-CVWPTYWNCG	$3.2 \cdot 10^{-5}$
J105	Ac-ACVWPTYWNCG	$4.5 \cdot 10^{-5}$
J109	ACVWPTYWACG	$2.0 \cdot 10^{-5}$
J110	ACVWPTYANCG	$2.4 \cdot 10^{-5}$
J111	ACVWPTAWNCG	$3.1 \cdot 10^{-5}$
J112	ACVWPAYWNCG	$3.3 \cdot 10^{-5}$
J113	ACVWATYWNCG	$5.5 \cdot 10^{-5}$
J115	ACAWPTYWNCG	$2.7 \cdot 10^{-6}$
J116	AAVWPTYWNAG	$3.4 \cdot 10^{-5}$
J117	ASVWPTYWNSG	$2.9 \cdot 10^{-5}$
J118	ACPYNWWTWCG	$2.9 \cdot 10^{-5}$
J119	ACVWPTYWnCG	$3.2 \cdot 10^{-5}$
J120	ACVWPTYwNCG	$3.4 \cdot 10^{-5}$
J121	ACVWPTYWNCG	$1.8 \cdot 10^{-5}$
J122	ACVWPIYWNCG	$5.1 \cdot 10^{-5}$
J123	ACVWpTYWNCG	$2.5 \cdot 10^{-5}$
J124	ACVwPTYWNCG	$2.0 \cdot 10^{-5}$
J125	ACvWPTYWNCG	$1.8 \cdot 10^{-5}$
J127	acvwptywncg	$4.4 \cdot 10^{-5}$
J128	gcnwytpwvca	$5.3 \cdot 10^{-5}$
J130	AEVWPTYWN(Dpr)G	$1.9 \cdot 10^{-5}$
J131	ACoWPTYWNCG	$5.5 \cdot 10^{-5}$
J132	AC(Leu)WPTYWNCG	$4.5 \cdot 10^{-6}$
J133	AC(dLeu)WPTYWNCG	$2.8 \cdot 10^{-5}$
J134	AC(Ile)WPTYWNCG	$7.4 \cdot 10^{-6}$
J135	AC(dIle)WPTYWNCG	$2.9 \cdot 10^{-5}$
J136	AC(Met)WPTYWNCG	$7.5 \cdot 10^{-6}$

FIGURE 8

J137	AC(dMet)WPTYWNCG	$2.5 \cdot 10^{-5}$
J138	AC(Abu)WPTYWNCG	$7.8 \cdot 10^{-5}$
J139	AC(dAbu)WPTYWNCG	$2.1 \cdot 10^{-5}$
J140	AC(Nva)WPTYWNCG	$3.6 \cdot 10^{-6}$
J141	AC(dNva)WPTYWNCG	$3.0 \cdot 10^{-5}$
J142	AC(tBuG)WPTYWNCG	$3.2 \cdot 10^{-5}$
J143	AC(dtBuG)WPTYWNCG	$3.8 \cdot 10^{-5}$
J144	AC(Phe)WPTYWNCG	$5.1 \cdot 10^{-6}$
J145	AC(dPhe)WPTYWNCG	$5.7 \cdot 10^{-5}$
J146	AC(Cha)WPTYWNCG	$2.2 \cdot 10^{-5}$
J147	AC(dCha)WPTYWNCG	$1.7 \cdot 10^{-5}$
J148	AC(Nal(1))WPTYWNCG	$5.8 \cdot 10^{-6}$
J149	AC(dNal(1))WPTYWNCG	$2.0 \cdot 10^{-5}$
J150	AC(Acy)WPTYWNCG	$2.0 \cdot 10^{-5}$
J151	ACVWPT(Hyp)WNCG	$2.2 \cdot 10^{-4}$
J154	ACVWPT(Nal2)WNCG	$8.2 \cdot 10^{-5}$
J155	ACVWPT(MetO <sub>2</sub> )WNCG	$1.9 \cdot 10^{-4}$
J157	ACVWPT(Cha)WNCG	$1.2 \cdot 10^{-4}$
J160	ACVWPT(Ser)WNCG	$1.8 \cdot 10^{-4}$
J162	ACVWPT(Thi)WNCG	$2.5 \cdot 10^{-4}$
J163	ACVWPT(dSer)WNCG	$5.0 \cdot 10^{-5}$
J166	ACVWPT(dCha)WNCG	$7.5 \cdot 10^{-5}$
J170	ACVWPT(dPhe)WNCG	$1.4 \cdot 10^{-4}$
J171	ACVWPT(Thr)WNCG	$7.7 \cdot 10^{-4}$
J174	ACVWPT(Phe)WNCG	$4.5 \cdot 10^{-5}$
J176	ACVWPT(dThr)WNCG	$2.8 \cdot 10^{-5}$
J180	ACVWPTYW D CG	$5.6 \cdot 10^{-5}$
J182	ACVWPT D WNCG	$2.7 \cdot 10^{-5}$
J183	ACVWP D YWNCG	$3.3 \cdot 10^{-5}$
J184	ACVW D TYWNCG	$6.2 \cdot 10^{-5}$

Figure 8 (Con't)



J185	ACV <sub>D</sub> PTYWNCG	$3.4 \cdot 10^{-5}$
J186	AC <sub>D</sub> WPTYWNCG	$3.5 \cdot 10^{-5}$
J187	ACVWTYWNPCG	$4.3 \cdot 10^{-5}$
J188	ACVWTYWPNCG	$3.0 \cdot 10^{-5}$
J189	ACVWTPYWNCG	$3.1 \cdot 10^{-5}$
J190	ACVWTPYWNCG	$2.6 \cdot 10^{-5}$
J191	ACVPWTYWNCG	$3.0 \cdot 10^{-5}$
J192	ACPVWTYWNCG	$4.2 \cdot 10^{-5}$
J193	ACWPTYWNVCG	$4.8 \cdot 10^{-5}$
J194	ACPTYWNVWCG	$4.2 \cdot 10^{-5}$
J195	ACTYWNVWPCG	$3.3 \cdot 10^{-5}$
J196	ACYWNVWPTCG	$2.4 \cdot 10^{-5}$
J197	ACWNVWPTYCG	$2.9 \cdot 10^{-5}$
J198	ACNVWPTYWCG	$4.2 \cdot 10^{-5}$
J199	ACVWPCG	$4.7 \cdot 10^{-5}$
J200	CVWPTYWNCG	$5.5 \cdot 10^{-5}$
J201	ACWWPTYWNCG	$6.8 \cdot 10^{-6}$
J202	ACEWPTYWNCG	$4.6 \cdot 10^{-6}$
J203	ACRWPTYWNCG	$5.8 \cdot 10^{-6}$
J204	ACQWPTYWNCG	$9.2 \cdot 10^{-6}$
J205	ACGWPTYWNCG	$4.4 \cdot 10^{-6}$
J207	cyclo-Valeroyl-AWPTYWNCG	$5.5 \cdot 10^{-5}$
J208	cyclo-ToluyI- AWPTYWNCG	$7.6 \cdot 10^{-5}$
J209	cyclo-Acetyl- AWPTYWNCG	$7.7 \cdot 10^{-5}$
J210	(WPTYWNCG) <sub>2</sub>	$5.3 \cdot 10^{-5}$
J211	(AWPTYWNCG) <sub>2</sub>	$7.9 \cdot 10^{-6}$
J212	ACA(Bpa)PTYWNCgK(biotin	$1.8 \cdot 10^{-5}$
J213	ACAWPTY(Bpa)NCGK(biotin	$1.8 \cdot 10^{-5}$
J214	GCAWPTYWNCG	$1.4 \cdot 10^{-6}$
J215	NCAWPTYWNCG	$9.0 \cdot 10^{-6}$

Figure 8 (Con't)

J216	VCAWPTYWNCG	$2.8 \cdot 10^{-6}$
J227	SFYEAHQLLGV-NH <sub>2</sub>	$6.4 \cdot 10^{-6}$
J228	HPPLEHLKAFLL-NH <sub>2</sub>	$2.4 \cdot 10^{-5}$
J229	APTFYAWFNQQT-NH <sub>2</sub>	$2.4 \cdot 10^{-6}$
S122	HPTSKEIYAKLLK	$9.3 \cdot 10^{-6}$
S123	HPSTNQMLMKLFK	$1.6 \cdot 10^{-5}$
S124	HPPLSELKLFLIKK	$2.3 \cdot 10^{-5}$

Figure 8 (Con't)

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
H5 Parental	LCQSLGVITYPGWLAGWCA	--	1.2	--	--
H5-3-JBA5-IGFR	LCQSWGVRIGWLAGLCP	31.9	16.3	--	--
H5-3-E1A11-IGFR	VCQSLGITDLGLCAGWGA	21.3	8.0	--	--
H5-3-E4B10-IGFR	LCQSLGLTHPGFEAWLCA	29.7	7.8	--	--
H5-3-E4C10-IGFR	LCQNFQVTDPGCFYGFWA	24.3	6.1	--	--
H5-3-JBB6-IGFR	PCQRLGDTLHCWLAGWFA	40.2	5.4	--	--
H5-3-E4A9-IGFR	LCQSSGLSFLGCLGWWA	27.7	4.3	--	--
H5-3-E2A12-IGFR	LCQSLGFTDLDLWACWFE	27.2	4.2	--	--
H5-3-E4A12-IGFR	VCQGLGVECPGWFAWGA	27.9	3.9	--	--
H5-3-E1F9-IGFR	PCQSLGLTCSGWFEWGA	18.6	3.5	--	--
H5-3-E4F11-IGFR	LCQGWGIRIGWLVGRM	28.4	3.3	--	--
H5-3-E4A11-IGFR	LWQSVGIKYPGGLAGWLA	31.0	3.0	--	--
H5-3-E4G7-IGFR	QWQSLGVTCPGSWAELCA	26.2	2.2	--	--
H5-3-E1B9-IGFR	LCQSLGVITYWEGLAWLCA	20.0	2.1	--	--

Figure 9A

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
JBA5 Parental	LCQSWGVRIGWLAGLCP	31.5	20.6	1.0	20.6	<0.1
JBA5-4-2C12-IGFR	LCQSWGVRIGWLAGLCP	46.8	41.5	1.0	41.5	<0.1
JBA5-2-1F9-IGFR	LCESWGVRIGWLAGLCP	48.1	39.5	1.0	39.5	<0.1
JBA5-2-1E10-IGFR	LCQSWGVRIGWLVGLCP	42.5	39.5	1.1	35.9	<0.1
JBA5-4-2A11-IGFR	LCQSWGVRIGWLAGLCP	44.1	40.2	1.2	33.5	<0.1
JBA5-3-2A3-IGFR	LCQSWGVRIGWLVGLCP	34.7	33.3	1.0	33.3	<0.1
JBA5-4-2A9-IGFR	LCQSWGVRIGWLTGLCP	34.6	33.1	1.0	33.1	<0.1
JBA5-1-1B6-IGFR	MCQSWDVRIGRLGGQCP	39.6	31.4	1.0	31.4	<0.1
JBA5-4-2B9-IGFR	LCQGWDRIGQLAGLCP	39.6	22.3	1.0	22.3	<0.1
JBA5-1-1H7-IGFR	LCQGWVRIGWLAGLCP	24.9	22.6	1.2	18.8	0.1
JBA5-3-2C3-IGFR	LCQSWDVRIGWVAGLCP	35.5	15.3	1.1	13.9	0.1
JBA5-1-1G7-IGFR	LCQSWDARIGWLAGLCP	26.2	14.8	1.5	9.9	0.1
JBA5-2-1E9-IGFR	LCLG*DVRIGLLAGLCP	39.4	4.5	1.0	4.5	0.2
JBA5-2-1D12-IGFR	L*KSWDVRSGLMAGLCP	42.2	2.2	1.0	2.2	0.5

Figure 9B

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR IR	IGFR/IR	IR/IGFR
JBA5-4-G12-IR	LCQSWGVRIGWLAGLCP	--	--	--	--
JBA5-4-G3-IR	LCQSWDACIQWLVLGLSP	37.5	3.0	1.4	2.1
JBA5-4-G1-IR	LCRSWECEIGWLVGPQP	4.5	2.5	1.1	2.3
JBA5-3-B1-IR	LCQSWGECIDRLVGQGA	32.0	3.2	1.3	2.5
JBA5-3-C1-IR	LCQGWGVRIGWLAGLCP	29.4	6.8	1.2	5.7
JBA5-3-A6-IR	LCQGWAVHIGQLAGLCP	36.3	7.5	1.1	6.8
JBA5-3-A2-IR	LCQGWGVHIGRLAGLCP	28.0	7.4	0.7	10.6
JBA5-3-B7-IR	LCQSWGVRIGWLAGLCP	10.2	4.8	0.4	12.0
	LCQSWGVRIGRLAGLCP	39.2	15.2	1.2	12.7
					0.1

Figure 9C

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
<b>Design</b>	XXXXXXXXXXXXXXXXXXXX	--	--	--	--
R20-4-C10-IGFR	PKGTRFRGDDVWDGYSWLA	37.8	3.8	--	--

**Figure 10A**

Clone	Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
20F-4-B7-IGFR		TPIPAGGINIASWGGYTWS	10.9	3.7	0.5	7.3	0.1
20F-4-E4-IGFR		HRGTVGVVVARWPGYEWLS	8.9	4.7	0.7	6.3	0.2
20F-4-E12-IGFR		SDVWAQPQRRNDWPGYHWLS	9.7	4.7	0.8	6.0	0.2
20F-4-F4-IGFR		HRGTVGVVVARWPGYEWLS	13.9	10.1	1.8	5.6	0.2
20F-4-F7-IGFR		SDVWAQPQRRNDWPGYHWLS	13.7	3.9	0.8	5.1	0.2
20F-4-E7-IGFR		RPHRINPQDDAVWPGYLWL	7.2	2.5	0.5	4.7	0.2
20F-4-F11-IGFR		HRGTVGVVVARWPGYEWLS	17.6	16.2	3.5	4.6	0.2
20F-4-D10-IGFR		FGRGYGGDGGYWSGYEWLA	9.8	2.4	0.6	4.1	0.2
20F-4-B3-IGFR		DGLVVKSGREWPGYCWLER.A	17.3	14.4	3.6	4.0	0.2
20F-4-B12-IGFR		DGSIV.VSSVGVWPGYEWLM	10.1	9.9	2.4	4.0	0.2
20F-3-A9-IGFR		WQANLSNGGGRWGGYDWLM	6.6	2.7	0.7	4.0	0.2
20F-4-G2-IGFR		FGRGYGGDGGYWSGYEWLA	5.1	1.3	0.5	2.7	0.4
20F-4-D11-IGFR		VNYEMDRVPPMPWGGYWWLS	5.0	1.0	0.5	2.3	0.4
20F-4-G4-IGFR		MGGGLWVGVIWPGYSWLSQ	3.9	0.9	0.5	1.8	0.6
20F-4-G12-IGFR		SDVWAQPQRRNDWPGYHWLS	3.2	0.9	0.6	1.5	0.7

Figure 10A (Con't)

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
<b>Design</b>	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20 $\beta$ -4-A4-IR	WPGYLFEEALQDWRGSTD	11.9	17.5	1.4	12.5	0.1
R20 $\beta$ -4-F2-IR	SMFVAGSDRWPGYGLADWL	16.4	13.9	3.1	4.5	0.2
R20 $\beta$ -4-E8-IR	VRGFQGGTVWPGYEWLRNAA	41.0	34.9	3.6	9.7	0.1



Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
20F-4-H10-IR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--
20F-4-C10-IR	LDLASGDSWLGYDVLRGWLS	10.2	3.1	1.3	0.8
	IHSSDGIGAWGGYAWFRDVA	23.4	9.6	2.3	0.4

Figure 10B (Con't)

# Figure 10C

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20β-4-D10-IR	LGPLLRWGSEVCGVWPDLC	21.5	1.0	8.0	0.1	8.0
R20β-4-D9b-IR	PFGGGRWWGIPRMWWYRNS	32.6	6.8	15.1	0.5	2.2
R20β-4-H4-IR	WWGGRNRWWLERWGLGGER	11.6	1.7	3.6	0.5	2.1
R20β-4-A2-IR	GRVALWGPVWPRWFMSPV	17.1	2.6	5.2	0.5	2.0

Figure 10C

# Figure 10D

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
R40-3-40A2-IR	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R40-4-40F10-IR	RGTRTDRLWKSGGFAIVPRWPCFSYHCLVEWITKTGSPG	44.6	1.5	2.7	0.6	1.8
	GRTSMAFVPPRHLQPELAPRPNHAWLVGGG	46.4	1.9	2.1	0.9	1.1

Figure 10D



Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20C-3-H3-IGFR	xxxxcxxxxxxxxxxxxxxxxxxxxx	--	--	--	--	--
20C-3-F4-IGFR	DHRLCGTDEYLMQDLFVRGLCRLIW	28.5	26.6	1.0	26.6	<0.1
20C-4-C10-IGFR	GLLFCQKQFTLAGLQPEAGCVSSSR	34.4	27.5	1.2	23.1	<0.1
20C-3-G5-IGFR	IWIACLDLRLRGQVWSSCRRRAPIG	35.5	24.4	1.3	19.2	0.1
20C-3-A2-IGFR	DWLRCLGVILSGGLTELANTGCVQG	29.3	21.1	1.1	18.7	0.1
20C-3-B4-IGFR	WFSFCLGGLLQAQEWVWGRDVGCI	33.9	18.3	1.1	16.9	0.1
20C-3-C6-IGFR	GYSWLRDVLMEKQALKREGSVGRQ	39.8	29.1	1.9	15.2	0.1
20C-3-E2-IGFR	FLTRLRLERLGLS*ERGEAGGPIAQA	34.8	20.9	1.4	14.9	0.1
20C-3-A3-IGFR	FSGFCMGLERLSQVSLGYCAGQGG	34.8	28.1	2.0	14.2	0.1
20C-3-B1-IGFR	ISFRCQLFVLAGMHPCPVDVGGEGF	33.7	14.3	1.2	12.4	0.1
20C-3-F5-IGFR	NTPNCSQDWGQESGFMAILLALTCK	30.2	9.8	0.9	11.2	0.1
20C-4-A7-IGFR	LQGFCELLATVTGTGLGCLDYQPI	35.5	31.9	3.9	8.2	0.1
20C-4-F8-IGFR	GSSICNLLARAQIVELALCEMGVQE	33.3	19.3	2.8	6.9	0.1
20C-4-G11-IGFR	LSFACLLSQLSGVLPDCLLGED	30.5	27.7	5.3	5.2	0.2
20C-3-E1-IGFR	GEHFCQLLMSLCGDDCGPVNCGGGS	24.7	13.3	2.8	4.7	0.2
20C-3-B6-IGFR	GWFECLLASLVLPQGRSRASAVC	34.0	5.1	1.6	3.1	0.3
	YRQECACSVGAVGFLCGLCLARSG	37.3	32.8	13.7	2.4	0.4

Figure 10F

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGF/IR	IR/IGF
40F-4-D1-IGFR	LSCLAYSRHGIWRPSTDLGLGRSVGEGSVSTRWRGYDWFE	4.9	4.6	0.3	13.1	0.1
40F-4-B1-IGFR	GLDHSDAVGVHLGFAWPA.ARGWEAGGLEDTWAGYDWL	4.1	3.0	0.2	13.1	0.1
40F-4-D10-IGFR	W.GYAWLS	4.9	4.5	0.4	11.7	0.1
40F-3-A3-IGFR	LSCLAYSRHGIWRPSTDLGLGRSVGEGSVSTRWRGYDWFE	2.6	2.0	0.3	7.9	0.1
40F-4-C4-IGFR	EAMAVGLQCPARFVRAAAHGDGGSWGQDHV.AWGGYWWLG	3.8	2.0	0.5	4.1	0.2

Figure 10F (Con't)

# Sequence

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
		<u>HLCVLEELFWGASLFGYCSG</u>	39.1	1.8	27.7	0.1	15.4
	F815-4-G11-IGFR	HFYVLVERLSGASLFGSGSA	34.6	7.9	1.0	7.9	0.1
	F815-3-D1-IGFR	HRFVREGLLWGAYQFCYCSG	14.9	1.0	2.0	0.5	2.0
	F815-4-C12-IGFR	FQSLLEELVWGAPLFRYGTG	35.2	1.0	2.0	0.5	2.0
	F815-4-A11-IGFR	HLSVLEELSWGASLFGQWAG	5.4	1.0	2.1	0.5	2.1

Figure 10G

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
NNKH-4-A9-IR		HLSVLEELSWGASLFGQWAG	5.4	1.0	2.1	0.5	2.1
NNKH-4-H4-IR		NLCRLEELAWGASLFGQWAG	16.3	1.0	2.7	0.4	2.6
NNKH-4-B3-IR		APVSTEELRWGALLFGQWAG	15.6	1.0	2.6	0.4	2.5
NNKH-4-E1-IR		HLSVLEERWWRESLFGQWAG	13.6	2.8	6.7	0.4	2.3
NNKH-4-E7-IR		HLSVLEERWWRAALFGQWAG	13.9	4.8	9.5	0.5	2.0
NNKH-4-G3-IR		HLSILEEQWWRESLFGQWAG	16.9	1.3	2.3	0.6	1.8
NNKH-4-B6-IR		HMSVEELSWWASLFGKQAG	11.3	1.3	2.3	0.6	1.7
NNKH-4-A10-IR		HLSELEERWWRATLFGQWAG	13.2	1.3	2.1	0.6	1.7
NNKH-4-A5-IR		HLSVLEELWWRESLFGQWAG	15.4	2.0	3.2	0.6	1.6
NNKH-4-F11-IR		HLSLLEEQWWRESLFGQWAG	14.6	4.6	6.9	0.7	1.5
NNKH-4-C9-IR		HLSVLEERWWRETLLFGQWAG	14.0	3.1	3.9	0.8	1.3
NNKH-4-D12-IR		HLSVLEEQWWRESLFGQWAG	14.3	2.3	2.9	0.8	1.3
NNKH-4-D10-IR		HLSVLEEQWW .ESLFGQWAG	12.0	1.4	1.7	0.8	1.2
NNKH-4-E5-IR		HLSVLEELWWREALFGQWAG	13.6	1.2	1.5	0.8	1.2
NNKH-2-A6-IR		HLSVLEERWWRATLFGWAG	14.5	1.4	1.6	0.9	1.1
NNKH-4-F6-IR		HL .VLEELLWGVSLFRQWAG	8.4	1.4	1.5	1.0	1.1
NNKH-4-C7-IR		HLSALEEQWWRATLFGQWAG	14.1	2.8	2.9	1.0	1.0
NNKH-4-F7-IR		HLSVLEERWWRATLLESQ	14.7	1.4	1.4	1.0	1.0
NNKH-4-F8-IR		HLSALEELWWRETLLFGQWAG	14.1	7.5	7.0	1.1	0.9
NNKH-4-E9-IR		HLSVLEELWWRESLFGKWAG	13.6	11.0	8.6	1.3	0.8
NNKH-4-E6-IR		HLSVLEEAWWRESLFGHWAG	15.5	7.9	6.0	1.3	0.8
NNKH-4-B7-IR		HMSEQEELWWRATLFGQWAG	18.2	3.8	2.7	1.4	0.7
NNKH-2-B3-IR		HLSVLEERWWRETLLFGWAG	16.5	12.9	8.2	1.7	0.6
		HRSVLKQLSWGASLFGQWAG	11.5	5.3	0.7	7.4	0.1

Figure 10H



Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
NNKH-2-C5-IGFR	NNKH-2-C5-IGFR	HLSVLEELSWGASLFGQWAG	5.4	1.0	2.1	0.5	2.1
NNKH-2-D9-IGFR	NNKH-2-D9-IGFR	HL*VLEELSWGASLVGQWAV	7.3	0.9	0.7	1.3	0.8
NNKH-2-H12-IGFR	NNKH-2-H12-IGFR	HLSVLEEL*LGASMFGLWAG	4.1	0.5	0.4	1.3	0.8
NNKH-2-D10-IGFR	NNKH-2-D10-IGFR	HLSVLKELSW*ASLFGQWAG	5.0	1.3	1.1	1.2	0.8
NNKH-2-G9-IGFR	NNKH-2-G9-IGFR	HLSALEELSWGASLFGQWAG	4.8	2.1	1.9	1.1	0.9
NNKH-2-C6-IGFR	NNKH-2-C6-IGFR	HLSVLAELS*GALLFGQWAG	1.9	1.4	1.3	1.1	0.9
NNKH-2-C7-IGFR	NNKH-2-C7-IGFR	RLSVLEQLSWGASLFGPWAG	18.2	1.0	0.9	1.1	0.9
NNKH-2-F11-IGFR	NNKH-2-F11-IGFR	HL*VLVQPSWGASLFGQWAG	21.8	1.3	1.3	1.0	1.0
NNKH-2-H3-IGFR	NNKH-2-H3-IGFR	HQSVLEELSR*ASLFGQWAG	6.7	1.3	1.4	0.9	1.1
NNKH-2-B8-IGFR	NNKH-2-B8-IGFR	DMSVLGGLSWGA*LFGQWSG	4.7	0.7	0.8	0.9	1.1
NNKH-2-B12-IGFR	NNKH-2-B12-IGFR	HLSVREGQLWRASMFGRWAG	17.5	3.7	5.2	0.7	1.4
NNKH-2-F9-IGFR	NNKH-2-F9-IGFR	QLSVLVEL*WGASLFGPWAA	1.2	1.0	2.9	0.3	2.9
		HLSVGEELSW*VALLGQWAR	3.7	0.6	2.1	0.3	3.5

Figure 10I

D Name	Clonal Name	Formula #	K <sub>d</sub> (μM) HIR	PO <sub>4</sub>	Fat Cell Assay	Activity	K <sub>d</sub> (μM) HIGFR	Ratio IGF/IR	Sequence
D101	20D3	1	0.51 0.27				13 11	25 41	KIGGGQHQDGNFYDWFVEALAKK (ε-biotin)
D102	20D1	1	1.2 0.97				7.4 16	6.2 16	KVLQARHGCDSSVSDCFYEWFAKK (ε-biotin)
D103	B8	1	0.74				15	20	KWSALLSVMDDTGFYAWFDDAVKK (ε-biotin)
D104	E7	1	20				>20	>1	KGISWALVRHVDRLLFYEFDLKK (ε-biotin)
D105	H8	1	2.8				12	4.3	KRDKPTDQEEQNSFYEFWRHKK (ε-biotin)
D106	20F1	1	0.97				6.2	6.4	KVFWNCRSQQLDFYEWVFEQAACK (ε-biotin)
D107	40G11	1	1.1	YES		Antagonist	9.7	8.8	KLESHYVVPQAAALDRLLFYSWFSKK (ε-biotin)
D108	3G11	1	2.3			Antagonist	19	8.3	KFYGWFSRQSLTPRDDWGLPKK (ε-biotin)
D109	20H1	1	3.6			Antagonist	12	3.3	KSAPGLVSNKQDGLFYSWFREKK (ε-biotin)
D110	G3	1	0.84			Antagonist	1.4	1.7	KRGGGTIFYEFWFSALRKHGAGKK (ε-biotin)
D111	D2	1	0.62				3.2	5.2	KDPERMQSDVGFYEFWFRAAVGGK (ε-biotin)
D112	IGFR C1 A65-4-C1	1	0.49 0.19			Neutral	0.05* 0.02*	0.1 0.1	DYKDCWARPCGDAAANFYDWFVQQASKK (ε-biotin)
D113	IGFR I2 A65-4-1+2	1	0.75		~20 μM	Agonist	5.4	7.2	DYKDVTFITSAVFIENFYDWFVRQVSKK (ε-biotin)
D114	IGFR A6	1	8.1			Neutral	>20	>2.5	SAKNFYDWFVKK (ε-biotin)
D115	IGFR D5	1	8.1				>20	>2.5	ADKNFYDWFMAAKK (ε-biotin)
D116	IGFR JBA5	9	4.4 cycli		>20 μM	Agonist	8.1	1.8	DYKDLCSQSWGVRIGWLGLCPKK (ε-biotin)
D117	IGFR I2C	1	0.70	YES	~20 μM	Agonist	6.1 5.1	8.6 8.5	FIENFYDWFVRQVSKK(ε-biotin)
D118	20E2	2	0.25	YES	~20 μM	Agonist	1.3	5.2	DYKDFYDAIDQLVRGSARAGGTRDKK (ε-biotin)
D119	20C11	2	0.25	YES	~20 μM	Agonist	13 2.5	2.9 0.8	KDRAFYNGLRDLVGA VYGAWDKK (ε-biotin)
D120	E8	10	0.37			Antagonist	2.2	5.9	KVRGFGGTVWPGYEWLRNAKK (ε-biotin)
D121	F2	10	1.1			Antagonist	7.4	6.7	KSMFVAGSDRWPGYGLADWLKK (ε-biotin)
D122	20A4 (A7)	6	1.2 1.0			Antagonist	>20 >20	>17 >20	KEIEAEWGRVRLVYGRVCVGGKK (ε-biotin)
D123	D8	6	0.55 1.3			Antagonist	16 >20	29 >15	KWLDQEWAWVQCEVYGRGCPSSK (ε-biotin)
D124	F8	4	0.04* 0.09*				8.2 >20	200 >200	KHLCLVLEELFWGASLFGYCSGKK (ε-biotin)
D125	IGFR E4	1	2.6				>20	>8	DYKDERSAAGFRGNFYDWFVAQVNKK (ε-biotin)
D126	IGFR D2C	1	1.4				18	13	LGENFYDWFVMQVRKK

Figure 11A

Clonal Name	D or S name	Motif	Sequence	IR-Kd	IR-IC <sub>50</sub> Blacore	IR-IC <sub>50</sub> FP-S175	PO <sub>4</sub>	Fat Cell Assay
20-E2	D118	B6	DYKIDFYDAIDQLVRSARAGGTRDK K-biotin	250 nM		2.8 nM	+	++
C1	D112	A6	DYKDCWARPCGDAANFYDWFVQQAS KK-biotin	490 nM			-	0
D8	D123	C-C 100P	KWL DQEWAWVQCEVYGRGCPSSK	550 nM			0	-
E8	D120	GROUP 6	KRGFGGTWPGYEWLRNA	370 nM			-	-
F8	D124	C-C 100P	KHL CVLEELFWGASLFGYCSGKK	40 nM			-	0
H2C	D117	A6	FHEIFYDWFVROQVSKK	700 nM	>5 µM	5 nM	++	++
KCF9			RLYYEWFWGQLEAQGRGGLS					
KC-G2		C-C-C	GLEQGCPCWVGLEVCRCGPS					
KCG7		B6	FYCGLEELSWGAAFLGYCSG		<1 µm			
NG-C2		B6	GNIGDMFYQLLSLVGRDMH					
NG-G33		A6	GLISQSPESFYDWFAGQVSDPWWCW		2-4 µM	4.2 nM	+++	
NG-G8		B6	VEGRGLFYDLRLQLARRQNG		>5 µM		-	
NG-G9		B6	RAMSFYDALVSVLGLCPKK-Biotin				-	
RP-1		A6	GSRPVHIEQFYEFVFDQLGL		1 µM		+	
RP-2		A6	RSEASFIVEFYFWFEEQLRS		1 µM		+	
RP-3		A6	GRFYGWFDQDAIDQLMPWGF		>10 µM		-	
RP-4		B6	PPWGARYDAIEQLVFDNL		5 µM		+	
RP-5		B6	AGVNAGFYRYFSTLIDWWDQGGK-Biotin		6 µM		-	
RP-6		B6 + C-C	TFYSCLASLLTGTPQNRGPWERCRRK-Biotin				++++	
RP-7		A6	AAVIEQFYDWFADQYKK					
RP-8		B6	QSFYDYIEELIGGEWKK		>5 µM		+	
RP-8#	S287	B6	QSFYDYIEELIGGEWEE					
RP-9		A6	GSLEISFYDWFERQLGKK			2.9 nM	++	
RP-10		B6	GSFYELQRLVGGEQKK		>10 µM		+	
RP-11		A6	QAPSNFYDWFVREWDKK		>10 µM		+	
RP-12		B6	DPFYQGLWEWLRESGKK					
RP-13		A6	ASGFPENFYDWFGRQLSLKK		>10 µM			
RP-14		A6	SACQFDCIENFYDWFARQKK					
RP-15		A6	SQAGSAFYAWFDQVLRVTKK					
RP-16		B6	V.DARDDIFUJLSEVTL					
RP-17		B6	QSDAFYSGLWALIGLSDGKK		>10 µM			
RP-18		B6	LQPCSGFYECIERLIGVKK					
RP-19		A6	LKDGFDYDFWQRLHLGSKK					
RP-20		B6	GSASFYDAIDRLRMRIKK					
RP-24		GROUP 6	WPGYLFEEALQDWRGSTD					
S167	S167	A6	AFYDWFACK	>20 µM	No Binding		-	
S173	S173	RB6	LDALDRLMRYFEERPSL	1.2 µM				-
S174	S174	RB6	PLAELWAYFEISEQGRSSAH	16 µM				0
S175	S175	A6	GRVDWLQRANFYDWFVAELG	230 nM	2.4 µM	0.9 nM	++	0
S176	S176	A6	NGVERAGTGDNFYDWFVAQLH	470 nM				+++

Figure 11B

Clonal Name	D or S. name	Motif	Sequence	IR-Kd	IR-IC <sub>96</sub> Blacore	IR-IC <sub>96</sub> FP-S175	PO <sub>4</sub>	Fat Cell Assay
S177	S177	B6	EIIWNTVDFFYFTLFEWLRESG	2.7 μM				+
S178	S178	B6	EIIWNTVDFFYQYFSELLRESG	130 nM				0
S179	S179	A6	QSDSGTVIDRFYGFWRDTWAS	540 nM				++
F8-C12	S224	C-C LOOP	FQSLLEELVWGAPLFRYGTG					
S225	S225	C-C LOOP	PLCVLEELFWGASLFGYCSCG					
D8-G1	S226	C-C LOOP	QLEEWAGVQCEVYGRCPSP					
S264	S264	A6	IQGWEPFYGFDDVVAQMFEF					
S257	S257	B6	RWPNFYGFESLITIFS					
S258	S258	B6	HYNAFYEFQVLLAETW					
S259	S259	B6	EGWDFYSYFSGLLASVT					

Figure 11B (Cont)

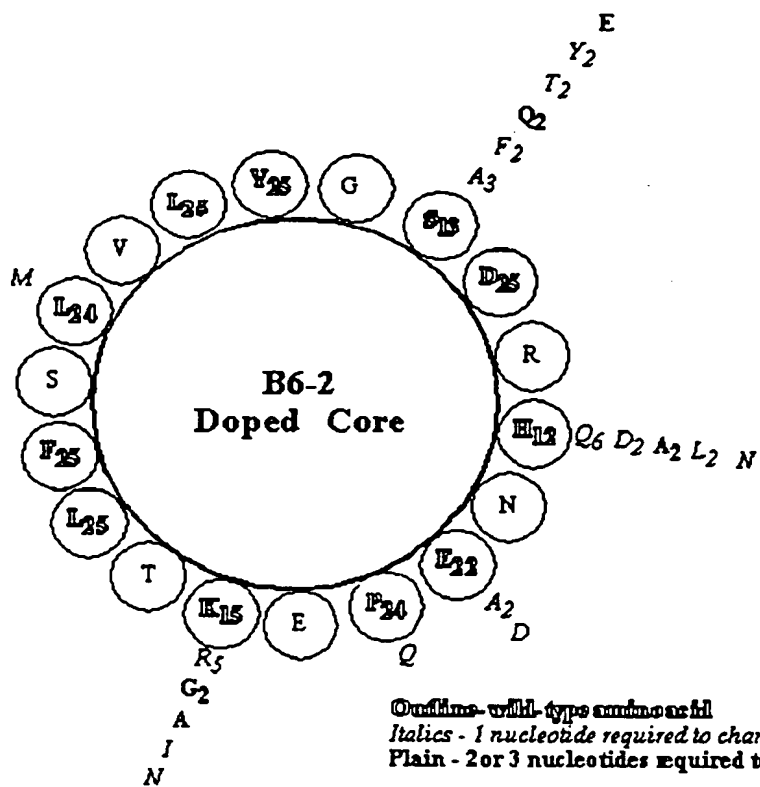


FIGURE 12

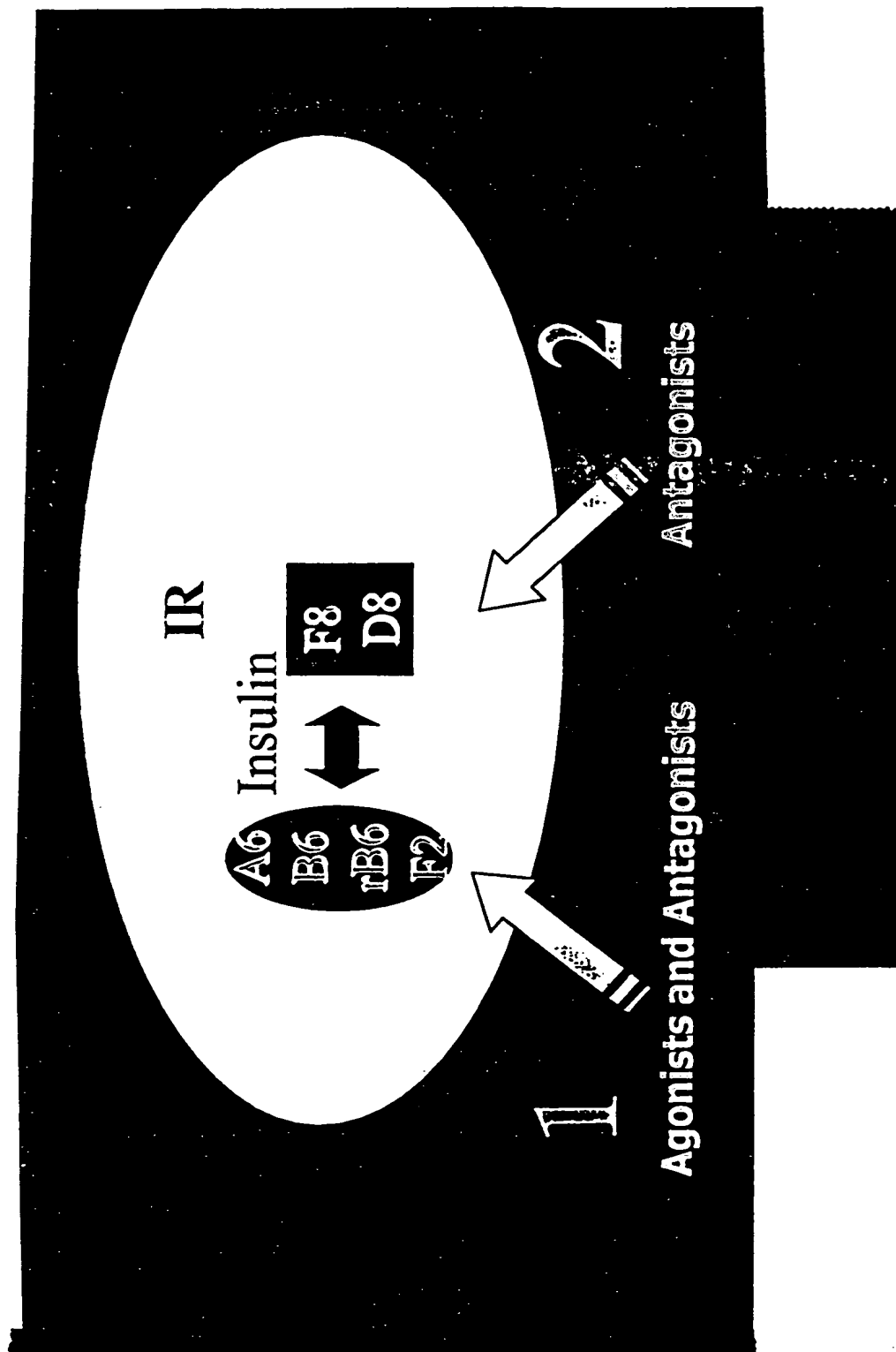


FIGURE 13

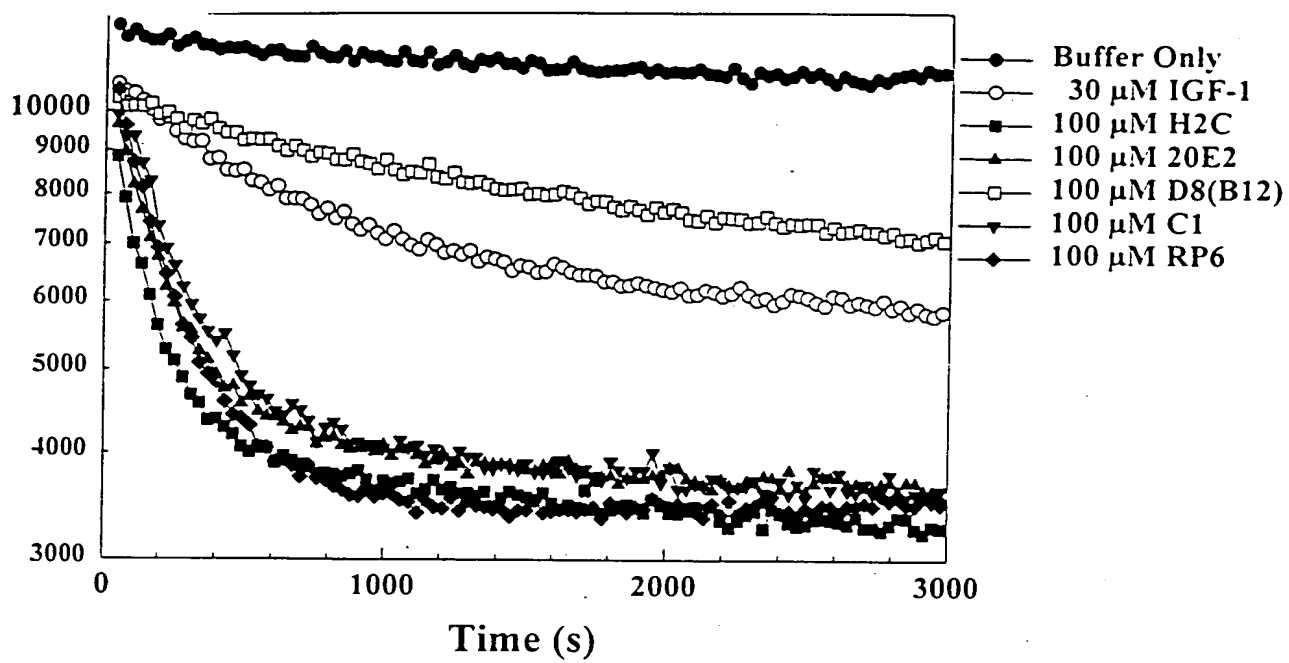


FIGURE 14





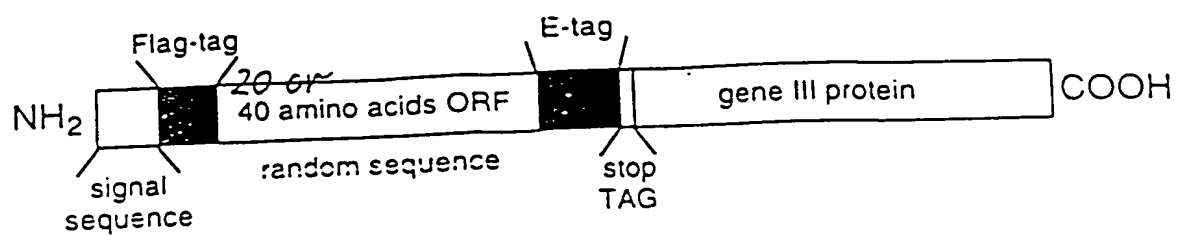


FIGURE 16

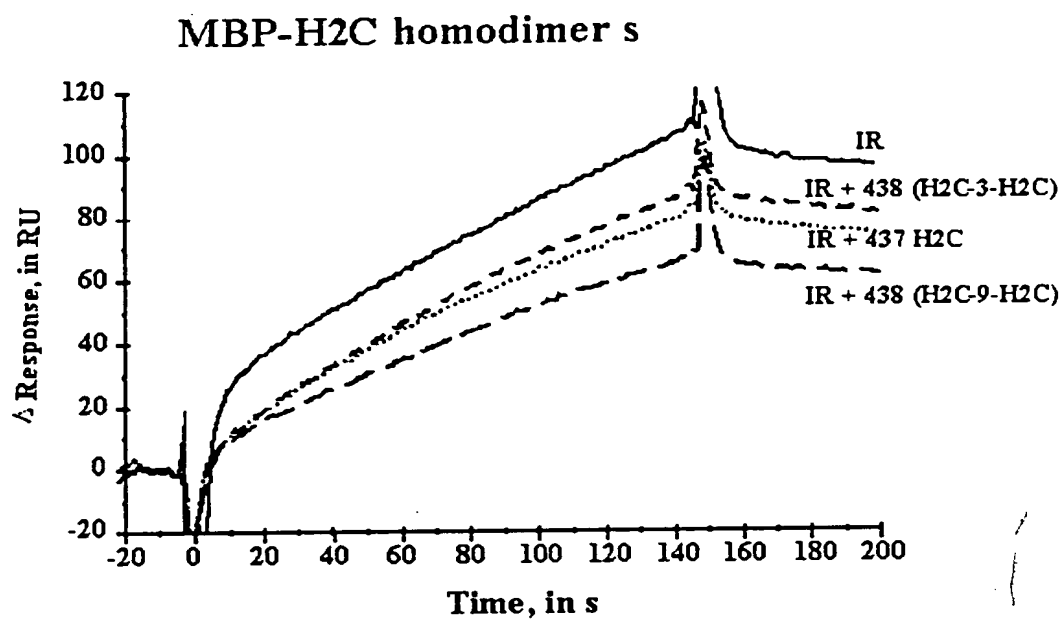


FIGURE 17

Class I clones		# Clones:		Compet-
		Rnd 3	Rnd 4	ition
B6 3x	DYKDAETPAQVGNRLWSVWPGEHWNTVDPFYHKLSELLRESGA	1	2	+
E5 2x	DYKDRHLTNAELGVQSPVLSRLFPDGDIFYRALSHLVGMGPP	2		+
B5 2x	DYKDRGGMDRQWLDVGARHRLERRSVQDNTDDFYGGRLRLVDGF	2		nd
9	DYKDGPPDSFDVTEKGDMAILNVRFDPHSLDFNDQTFYFLDLSL		1	nd
G6	DYKDGCTYFRGQVAQSNESLLRVNLFQLLEALAASPPT		1	nd
12	DYKDAPLDARLSAPRFQWSPRTWRQSLSYGEWSCGYDCLSSI		1	nd
A5	DYKDMGSSQFQDTRPSSGQAYSHSLSDSGWTANWIFLRALEGL		1	nd
C6	DYKDSGAHIEGNQGRERSTHLAANINDHLPDAGIWLGYSWLS		1	+
Consensus (regular+frameshifters) d.FY.11saL				
human IGF mature				
VCGRGFFYFNKPTGYGSSSR				
human IGF propeptide				
MSSSHLFYLAALCLLTFTSSA				
Class I frameshifting clones (all in +1 frame)				
F6 2x	TTKTRG.IFGMLLGVLRFQILLWFPKDCVQMKDIFYSLLASL	1	1	+
7 3x	TTKTRIGCCS.LVWGWRCRLADGFYAFMLALAG		3	nd
8	TTKTRLRLLLLGDEPFYGLRLMLIGRS		1	nd
G5	TTKTGWFAWV..LAFSVQGVGVAFYSALAALLCAHSASLVCGA	1		nd
Class II clones				
D5	DYKDPLYGGGIHLIYPGTMGVPGFPQVKVLGDADKNFYDWFEM	1		nd
A6	DYKDYRGMVLGRISDGAGKVASEPPPARIGQKVFVNFYDWFV	1		nd
R35	DYKDSGCCRLGLRLWMFIVVGWSGALVCQSAASAAGFYDWFV	1		
human IGF mature (1-70)				
GPETLCGAEL VDALQFVCGD RGEYFNKPTG YGSSRRAPQ TGIIVDECCFR SCDLRRLEMY CAPLKPAKSA				

nd = no data

FIGURE 18

# IGF-5

GACTACAAAG ACTGGTGGT GAATTTTCGG TAATGTCCTG GCGGTCTTCA GGTTCAGAT TCTTCTGCGG CCGTTCTTCA AGATTGCTG TCACATGAAA GATATTTT ATTCGTGTT GGTAGTTTG GCGGCCGCA 139  
D Y K D S M L N F R Y V A G R A Q V S D S S V A V S . G L C S D E R Y F L F V V G Q F G G R  
T T K T R G . I F G M L L G V L R F Q I L L M P F P K D C V Q M K D I F Y S L L A S L A A A  
L Q R L V V L F S V C C W A C L G F R F F C G R F L R I V F R . K I F F I R C W L V W R P

# IGF-6

GACTACAAAG ACCGGTGGT GCGTCTGCTT GCTCTTGGG GGTGATGAC CTTTATATGG GCTTCTCGT ATCGTATGG GTCTGCGGTC TCGGCCGCA 100  
D Y K D A V A A A V A P W G . . A F L M A S P Y A D W S W V C G R  
T T K T R L R L L L L L G G D E P F Y G L L R M L I G R G S A A A  
L Q R R G C G C C C S L G V M S L F M G F S V C . L V V G L R P

# IGF-Q5

GACTACAAAG ACTGGTGGT TTGCTTGGT GTGATGATTA GCTTTTCTG TTATAGGGGT CCGTGGCT TTTTACTAG CCGTGGCTG CTTGTGCTG TCCCATAGT CTTCCTTGT GTGTGCTG GCGGCCGCA 139  
D Y K D W L V C L G V M I S F F C L G G R C G F L L S V G C L V V C P Q C F F G V W C G G R  
T T K T G W F A W V . . L A F S V Q G V G V A F Y S A L A A L L C A H S A S I V C G A A A  
L Q R L V G L L G C D D Q L F L F R G S V M L F T Q R W L P C C V P I V L L M C V V R R P

# IGF-7

GACTACAAAG ACCGGTGGT GGTGTTGAG CTGATGAT TTGGGTGGA GCGGTATG ATGGCTGAT GGGTTTATG CCGTCTGCT GCGGCCGCG CA 112  
D Y K D P D W V L Q L I S L G L E G M Q I G . W V L C V F D G A G W G G R  
T T K T R I G C C S . L V W G W R G C R L A D G F Y A F L M A L A G A A A  
L Q R P G L G V V A D Q F G V G G D V D W L M G F M R F . W R M L G R P

FIGURE 19

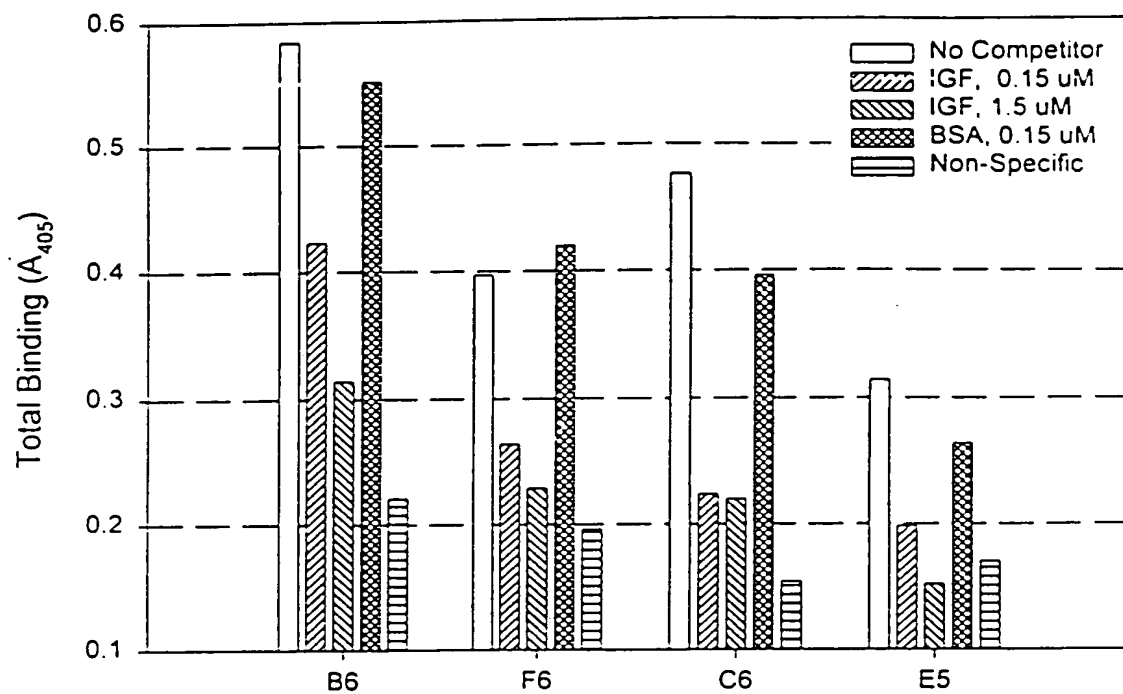


FIGURE 20A

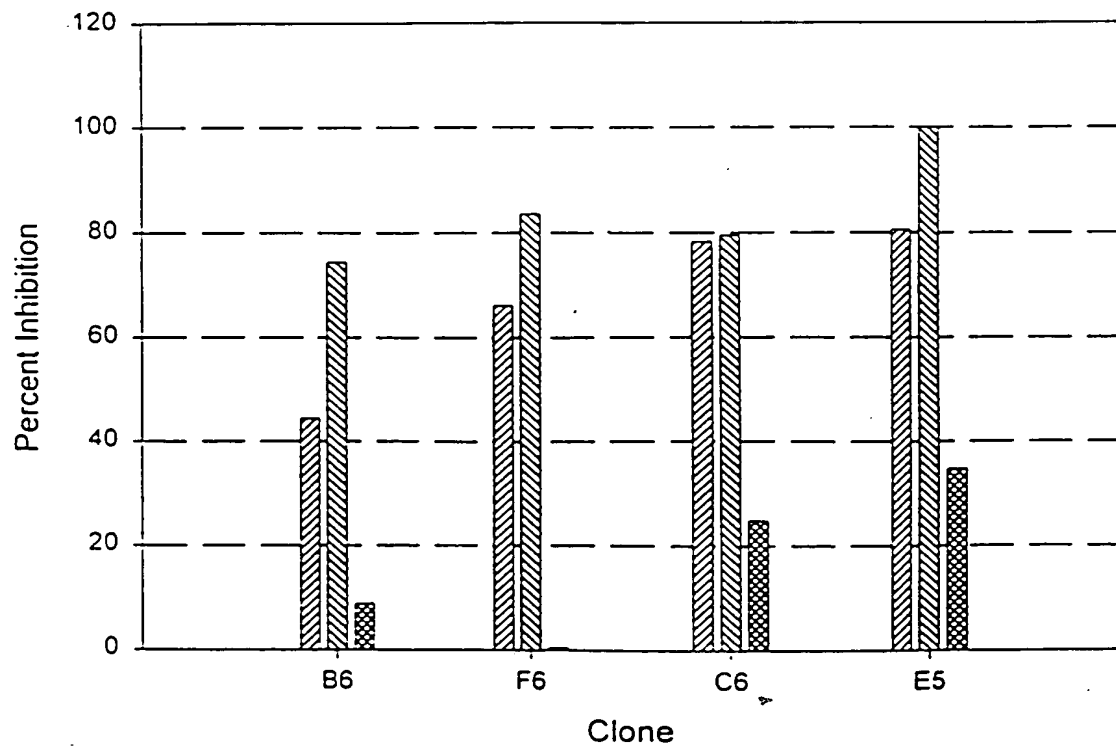


FIGURE 20B

SEQUENCE

Clone B6

AETPAQVGNRLWSVWPGEHWNTVDPFYHKLSELLRESGA

Peptide 5.1 (18 aa)

NTVDPFYHKLSELLREKK (biotin)

Clone F6

MLLGVLRFQILLWPFPPKDCVQMKDIFYSLLASL

Peptide 5.2 (17 aa)

QMKDIFYSLLASLAAKK (biotin)

Clone D5

PLYGGGIHLYPGTMGYVPGFPRQVKVLGDADKNEFDWFM

Peptide 5.3 (14 aa)

ADKNEFDWFMAAKK (biotin)

Clone A6

YRGMLVLGRISDGAGKVASEPPARIGQKVFVNEFDWFEV

Peptide 5.4 (12 aa)

SAKNEFDWFEVKK (biotin)

FIGURE 21

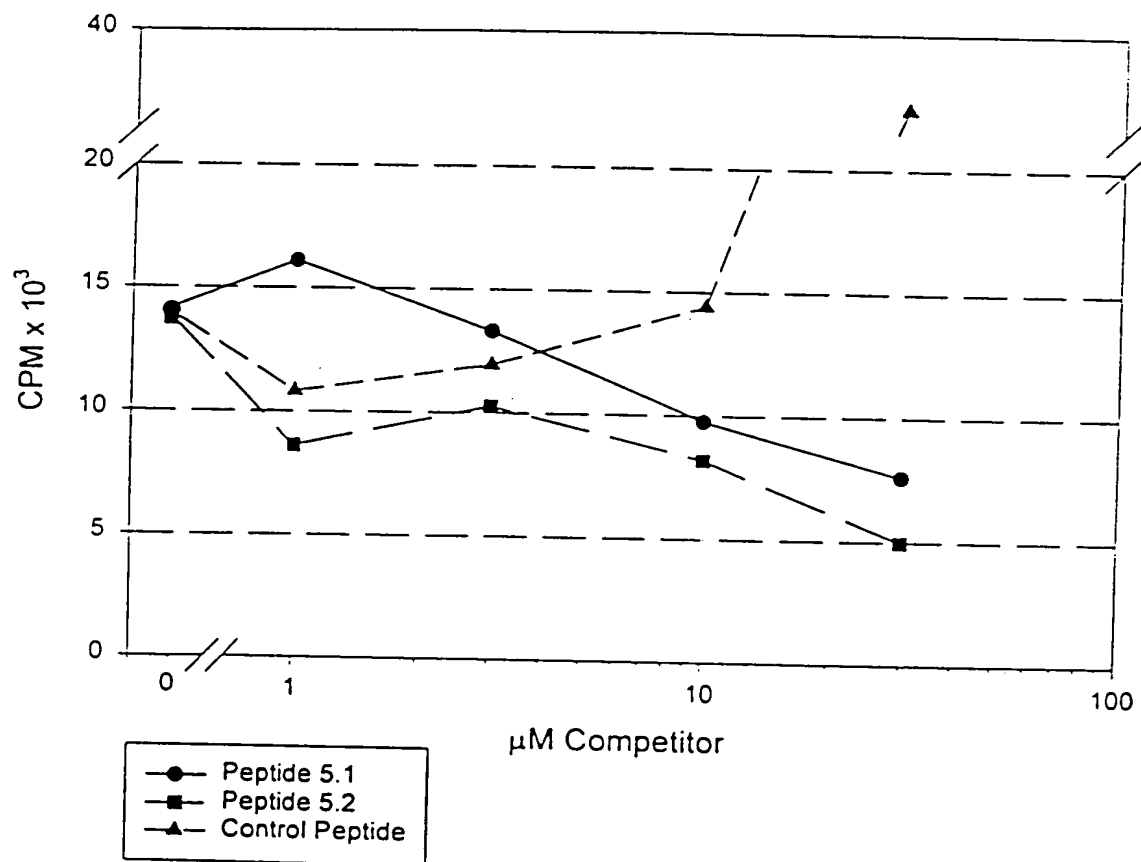


FIGURE 22

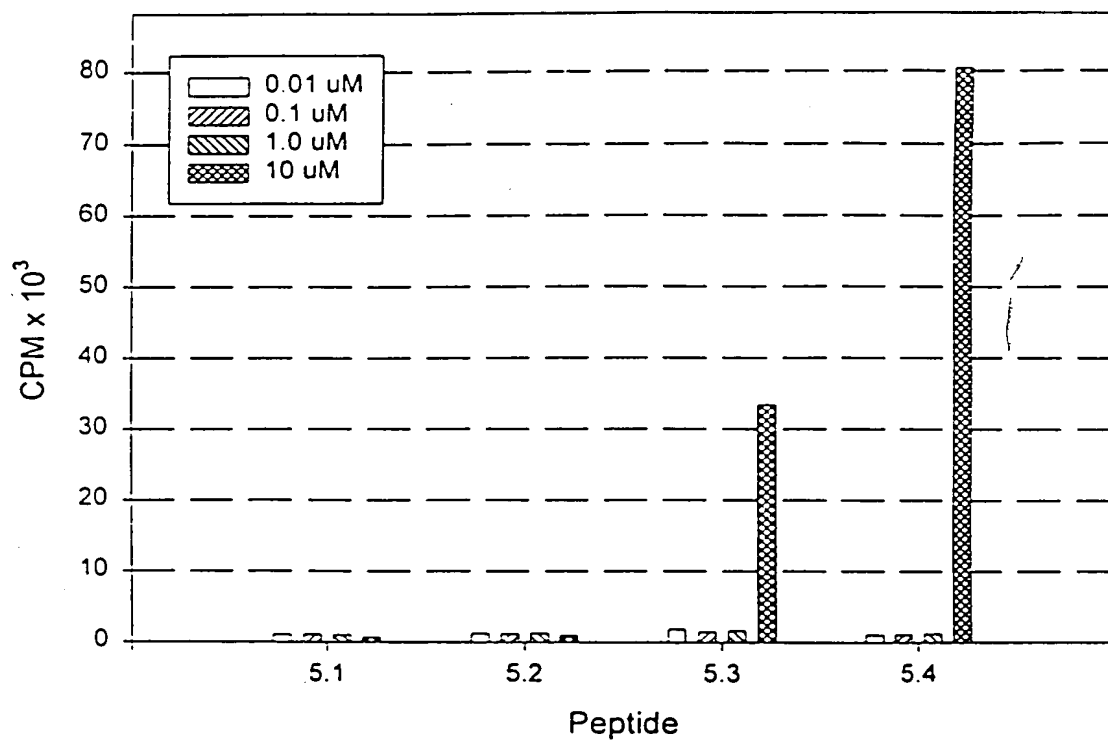


FIGURE 23



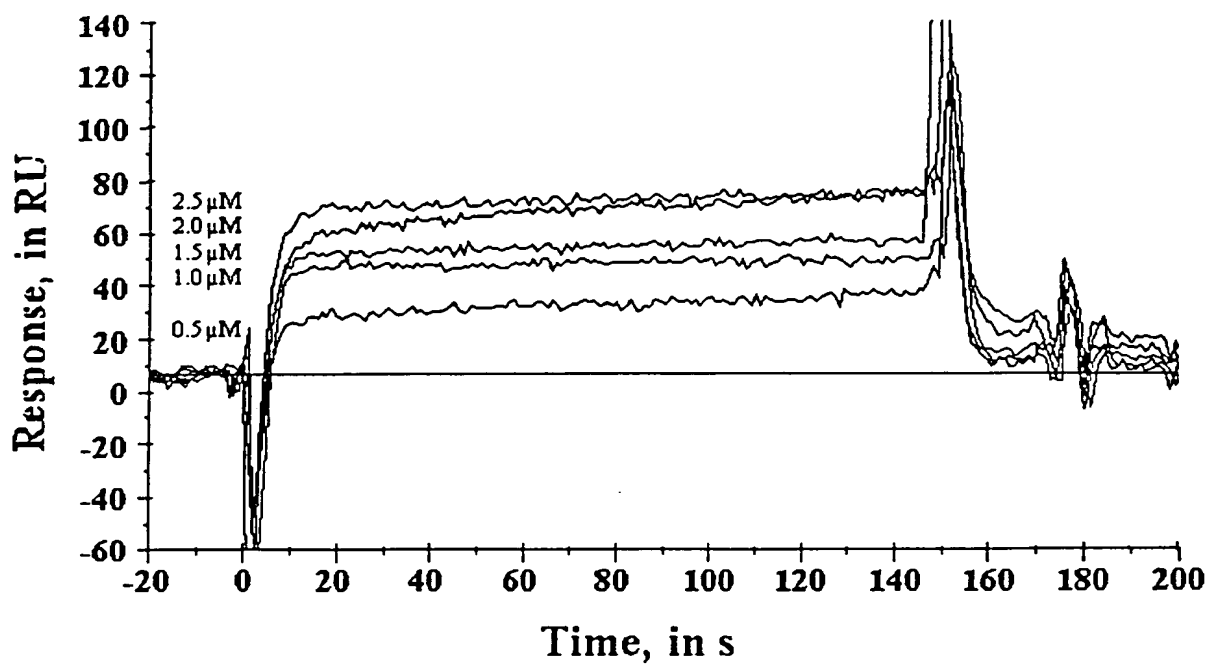


FIGURE 24A

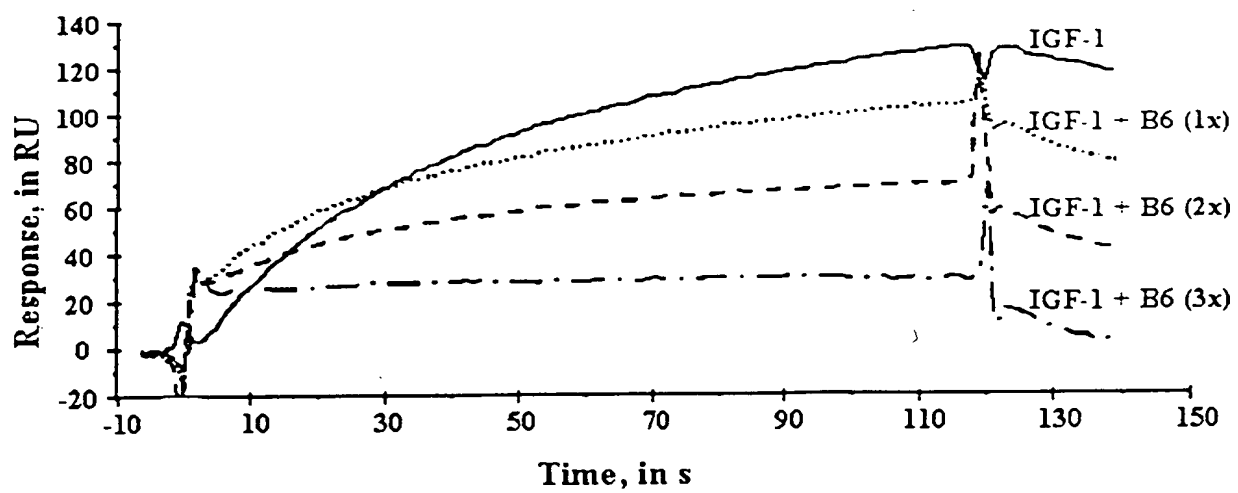


FIGURE 24B

GACTACAAAGACGACGATGACAAGTACCGTGGTATGCTGGTTCTGGGTCGTATCTCTGACG  
D Y K D D D D K Y R G M L V L G R I S D

GTGCTGGTAAAGTTGCTTCTGAACCGCCGGCTCGTATCGGTCAGAAAGTTTTCGCTGTTAA

G A G K V A S E P P A R I G Q K V F A V N

CTTCTACGACTGGTTCGTTGCGGCCGCA 96 nt  
F Y D W F V A A A

FIGURE 25A

CTACAAAGACGACGATGACAAGTACCGTGGTATGCTGGTTCTGGGTCGTATCTCTGACGGTGCT  
GGTAAAGTTGCTTCTGAACCGCCGGCTCGTATCGGTCAGAAAGTTTTCGCTGTTAACTTCTACG  
ACTGGTTCGTTGCGGCCGCAAGTGTGA 154 nt

FIGURE 25B

005252-222553

TTNNKNNKNNKNNK 21 aa  
V X X X X

CTACAAGACNNKNNKNNKNNKNNKNNKNNKNNKNNKA ACTTCTACGACTGGTTTCGTNNK  
NNKNNKNNKGCGGCCGCAGTGTGA

FIGURE 26B

1. The first part of the paper is devoted to the study of the properties of the function  $f(x)$  defined by the equation  $f(x) = \sum_{n=0}^{\infty} a_n x^n$ , where  $a_n = \frac{1}{n!}$ . It is shown that  $f(x)$  is a continuous function on the interval  $[0, 1]$  and that it is differentiable at  $x=0$ . The derivative of  $f(x)$  at  $x=0$  is equal to 1.

H5	NH <sub>2</sub> -D-Y-K-D-L-C-Q-S-L-G-V-T-Y-P-G-W-L-A-G-W-C-A-K-K(Biotin)-COOH
H5 Control	NH <sub>2</sub> -D-Y-K-D-W-C-L-T-L-Q-F-L-V-W-A-S-G-G-G-Y-C-A-K-K(Biotin)-COOH
2C3-60	NH <sub>2</sub> -D-Y-K-D-V-C-Q-R-L-G-G-T-F-P-G-W-L-V-G-V-C-R-K-K(Biotin)-COOH
H5-447	NH <sub>2</sub> -D-Y-K-D-L-C-Q-R-L-G-V-G-W-P-G-W-L-S-G-W-C-A-K-K(Biotin)-COOH
H5-432	NH <sub>2</sub> -D-Y-K-D-L-C-Q-S-L-G-V-T-W-P-G-W-L-A-G-W-C-A-K-K(Biotin)-COOH

FIGURE 27

1. The first group of people who are interested in the study of the history of the United States are the people who are interested in the history of the United States.

Clone:

Binding Ratios:  
Target E-Tag % Max

A6S-1-C5	DYKD	RIHNQTERCGNFYDWFVHqLV	AAA	7	27	26
A6S-1-G3	DYKD	VATVHVGGGMNFYDWFVAqVG	AAA	5	19	26
A6S-1-A2	DYKD	KDPVTVSQGRNFYDWFVqIQ	AAA	5	20	25
A6S-1-D5	DYKD	RVGSGMEDLGNFYDWFVRQAq	AAA	5	25	20
A6S-1-H4	DYKD	HKSWTTMSPLNFYDWFVAqVE	AAA	3	18	17
A6S-2-F2	DYKD	LAMSVASRPANFYDWFVAqIV	AAA	30	35	86
A6S-2-D2	DYKD	RAERGSMRDSNFYDWFVqQLP	AAA	30	36	83
A6S-2-E3	DYKD	VqEGLSGMEGNFYDWFVDQLF	AAA	28	36	78
A6S-2-H2	DYKD	RGqRESDSGTNFYDWFVGAI R	AAA	28	40	70
A6S-2-A3	DYKD	SRAPYGSTAGNFYDWFVqAVS	AAA	25	37	68
A6S-2-H1	DYKD	RVGIqVDPHTNFYDWFVIQLT	AAA	27	42	64
A6S-2-F1	DYKD	VGqVGRYVRSNFYDWFVQqAM	AAA	8	30	27
A6S-2-G1	DYKD	RPqLVESGSKNFYDWFVqVVR	AAA	8	30	27
A6S-2-B2	DYKD	EMYGDTSERVNFYDWFVSALq	AAA	5	30	17
A6S-2-A1	DYKD	LSSRGRVTMRNFYDWFVAqVV	AAA	3	31	10
A6S-3-E1	DYKD	RVREKLPRPENFYDWFVNqIH	AAA	22	23	96
A6S-3-G2	DYKD	TWMWEERKqDNFYDWFVGQLK	AAA	20	21	95
A6S-3-E5	DYKD	RYRGERHDGRNFYDWFVEqVN	AAA	19	21	90
A6S-3-H2	DYKD	qGAEGRLSEGNFYDWFVQAVS	AAA	19	21	90
A6S-3-H9	DYKD	YSIEVqDWNENFYDWFVSQLG	AAA	20	23	87
A6S-3-G3	DYKD	PRLHMGSDMGDFYDWFVqIA	AAA	18	21	86
A6S-3-F8	DYKD	GRGqGLKRPDNFYDWFVAAAK	AAA	20	25	80
A6S-3-G1	DYKD	GAVGLAEAGPNFYDWFVSqVq	AAA	19	24	79
A6S-3-H1	DYQD	PASNKNSLAENFYDWFVqQTR	AAA	23	30	77
A6S-3-E6	DYKD	DARDHGVVMSNFYDWFVAqVS	AAA	5	20	25
A6S-3-D9	DYKD	SLOGADFqQGNFYDWFVSELA	AAA	4	17	24
A6S-3-E3	DYKD	RPSLPEVRPGNFYDWFVqSVR	AAA	4	19	21
A6S-3-H8	DYKD	NPTSVqQYGVNFYDWFVNVLS	AAA	4	20	20
A6S-3-G4	DYKD	CADPGACSSLNFYDWFVqMRG	AAA	4	21	19
A6S-3-B1	DYKD	YDqDPPYWGLNFYDWFVREVA	AAA	3	16	19
A6S-3-C1	DYKD	RPVIGGGGTRNFYDWFVAqMI	AAA	3	17	18
A6S-4-G5	DYKD	QEVTRTRDDKNFYDWFVSqIF	AAA	26	18	144
A6S-4-D2	DYKD	PPYRSSRLGENFYDWFVMqVR	AAA	26	19	143
A6S-4-F6	DYKD	LKGSSQPLSVNFYDWFVQQIK	AAA	24	17	142
A6S-4-H4	DYKD	PRMVEKPSEDNFYDWFVTqLS	AAA	28	20	141
A6S-4-C1	DYKD	CWARPCGDAANFYDWFVqQAS	AAA	22	16	141
A6S-4-G3	DYKD	GAQAIREIHNFYDWFVAQVT	AAA	29	21	139
A6S-4-H3	DYKD	GRGDQRHETT NFYDWFVRELq	AAA	28	20	137

FIGURE 28

A6S-4-H6.	DYKD	GSIAQLIMRANFYDWFVEqTN	AAA	24	18	130
A6S-4-G6	DYKD	RLMGGIAEPqNFYDWFVREVA	AAA	25	20	126
A6S-4-H5	DYKD	HHSPGNEHGYNFYDWFVLqVA	AAA	24	19	123
A6S-4-E4.	DYKD	ERSAAGFREGNFYDWFVAqVN	AAA	32	27	120
A6S-4-F5.	DYKD	GSQHSGREPHNFYDWFVAqVG	AAA	28	24	120
A6S-4-D4	DYKD	IARMRETFQPNFYDWFVDQLA	AAA	21	18	118
A6S-4-C6	DYKD	RLDRSSTSGVNFYDWFVAqVG	AAA	28	25	116
A6S-4-D3	DYKD	GLRSEQGNRLNFYDWFVAQIA	AAA	23	20	116
A6S-4-F2	DYKD	SVIQTRQDETNFYDWFV?AMS	AAA	26	23	115
A6S-4-A5	DYKD	VEVQRHIRKDNFYDWFVKQID	AAA	22	19	115
A6S-4-C3	DYKD	VTMLDKGAQDNFYDWFVREVA	AAA	24	21	114
A6S-4-F3	DYKD	HNSSSPMRTGNFYDWFVQELR	AAA	30	26	113
A6S-4-B4	DYKD	ERSPRPALASNFYDWFVQQVV	AAA	21	19	113
A6S-4-B6	DYKD	SDARQAGLQENFYDWFVSQVR	AAA	26	23	113
A6S-4-B1	DYKD	RHERGKEGPGNFYDWFVSQVV	AAA	21	19	112
A6S-4-G4	DYKD	SALSGPVqPINFYDWFVTGM	AAA	30	26	112
A6S-4-A6	DYKD	HVEHMAVGDGNFYDWFVVqLR	AAA	23	21	111
A6S-4-F4	DYKD	VGHSGVPPYPNFYDWFVMQVS	AAA	24	22	110
A6S-4-D6	DYKD	LGAAETWDGINFYDWFVKQVS	AAA	24	22	110
A6S-4-E6	DYKD	RSSGGLLSqGNFYDWFVSQLE	AAA	26	24	109
A6S-4-A3	DYKD	LAINDLVTHKNFYDWFVDQLR	AAA	20	18	109
A6S-4-E3	DYKD	RGMTGMVGRGNFYDWFVGQLR	AAA	23	21	109
A6S-4-A2	DYKD	IGGQGHQDGNFYDWFVEALA	AAA	22	20	107
A6S-4-B2	DYKD	QSVDLSRPDSNFYDWFVEVLS	AAA	22	21	105
A6S-4-H2	DYKD	VTFTSAVFHENFYDWFVRQVS	AAA	20	19	104
A6S-4-D1	DYKD	SNPSRQDASVNFYDWFVREVA	AAA	22	22	103
A6S-4-H1	DYKD	IVAGARHSEVNFYDWFVIQVR	AAA	18	18	102
A6S-4-E2	DYKD	?DGQSVSSKGNFYDWFVQqMT	AAA	25	25	101
A6S-4-G1	DYKD	AELVGAGVRGNFYDWFVDQLV	AAA	16	16	101
A6S-4-G2	DHKG	SAGHHMPRESNFYDWFVDQVV	AAA	24	25	99
A6S-4-A1.	DYKD	DSSRLWLGERNFYDWFVAqIS	AAA	12	17	68

FIGURE 28 (Cont.)

Name	Sequence	#Found	Ratio	IGF Inh.	GHR*
H5:	LCQSLGVTPGWLAGWCA	-	1.2	-	2.0
2C3:	VCQRLGGTFPGWLVGVCR	-	1.1	-	1.1
JBA5:	LCQSWGVRI-GWLAGLCP	19	~24.0	~45%	1.2
E2A12:	LCQSLGFTDLDWLACWFE	10	~17.5	~54	1.1
E1A11:	VCQSLGITDLGLCAGWGA	1	16.4	50	1.0
E4B10:	LCQSLGLTHPGFEAWLCA	5	~11.7	~50	1.2
E4C10:	LCQNFQVTDPGCFYGWFA	1	9.9	~51	0.7
E4A9:	LCQSSGLSFLGCL-GWWA	14	~8.5	~65	1.0
JBB6:	PCQRLGDTHLCWLAGWFA	6	~8.3	~65	1.1
E1F9	PCQSLGLTCSGWFEWGA	1	8.3	68	1.2
E4G7:	QWQSLGVTCPGSWAELCA	1	6.0	50	1.3
E4A11:	LWQSVGIKYPGGLAGWLA	1	5.8	67	1.4
E1B9:	LCQSLGVTYWEGWLAWLCA	3	5.5	60	1.1
E4A12:	VCQGLGVECPGWFAWWA	3	~5.3	~55	1.2
E4F11:	LCQGWGIRI-GWLVGRCM	1	2.7	58	1.1
E1D3:	LCQSLGVTPGWLAGGCA	1	2.0*	-	1.0

FIGURE 29



# Genomic rVab Library

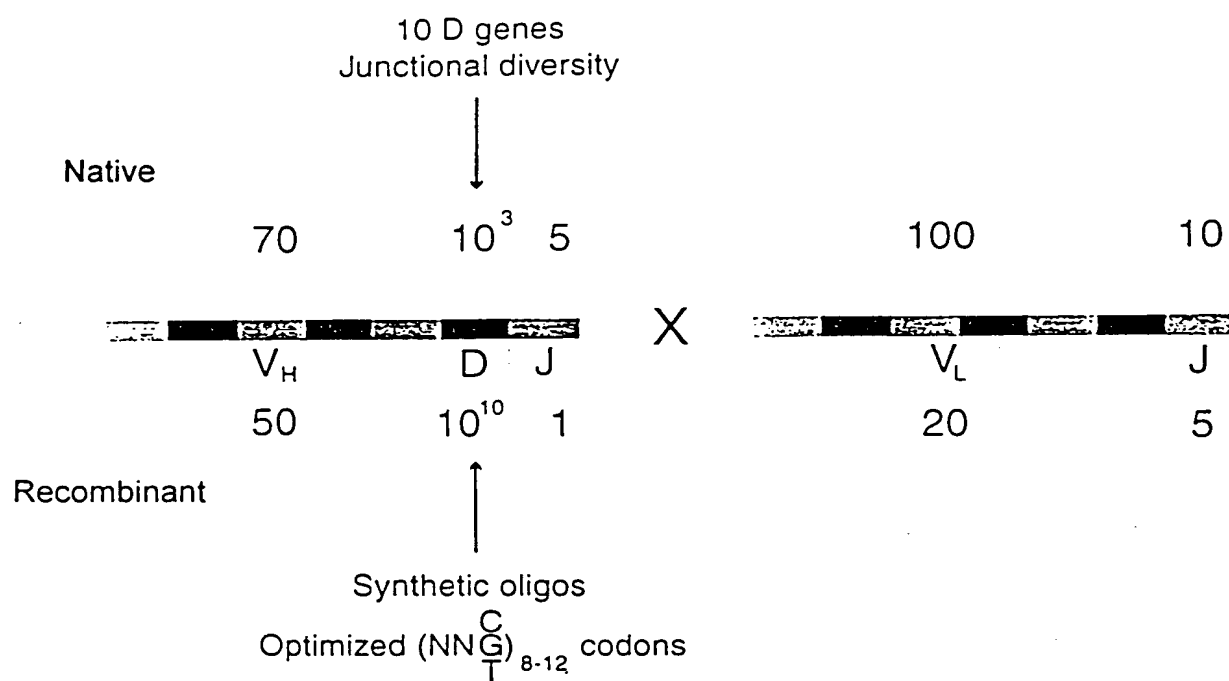


FIGURE 30

# VH Gene Sequences

DP-1  
DP-10  
DP-12  
DP-14  
DP-15  
DP-2  
DP-21  
DP-25  
DP-29  
DP-30  
DP-31  
DP-32  
DP-33  
DP-35  
DP-38  
DP-39  
DP-40  
DP-42  
DP-44  
DP-45  
DP-46  
DP-47  
DP-5  
DP-50  
DP-51  
DP-52  
DP-53  
DP-54  
DP-59  
DP-63  
DP-66  
DP-67  
DP-68  
DP-69  
DP-7  
DP-70  
DP-71  
DP-73  
DP-74  
DP-8  
hv1263  
VHD26

# Lambda and Kappa Gene Sequences

DPK11  
DPK15  
DPK18  
DPK2/L14+  
DPK3/L11+  
DPK4  
DPK6  
DPK8/Vd+  
DPL23  
HK101  
L22+  
L23/L23a  
LFVK431  
VA++

FIGURE 31



EcoRI / SfiI / VII gene / CDR III / JHb gene / C45 linker /  
 CCGGAATTTCGCGCCAGCGCCNNNN-----HAA  
 GGCCTTAAGCCGCGTCCGCGNNNN-----N  
 3' end for 7 VII genes: DP31, DP33, DP39, DP40, DP47 and DP49  
 GGCCTTAAGCCGCGTCCGCGNNNN-----N  
 3' end for 40 VII genes  
 CCGGAATTTCGCGCCAGCGCCNNNN-----HAA  
 GGCCTTAAGCCGCGTCCGCGNNNN-----N  
 3' end for 7 VII genes: DP31, DP33, DP39, DP40, DP47 and DP49  
 CCGGAATTTCGCGCCAGCGCCNNNN-----NCA  
 GGCCTTAAGCCGCGTCCGCGNNNN-----N  
 3' end for 4 VII genes: DP2, DP3, DP5 and DP38

CCGGAATTTCGCGCCAGCGCCNNNN-----HAA  
 GGCCTTAAGCCGCGTCCGCGNNNN-----N  
 3' end for 7 VII genes: DP31, DP33, DP39, DP40, DP47 and DP49  
 CCGGAATTTCGCGCCAGCGCCNNNN-----NCA  
 GGCCTTAAGCCGCGTCCGCGNNNN-----N  
 3' end for 4 VII genes: DP2, DP3, DP5 and DP38

CCGGAATTTCGCGCCAGCGCCNNNN-----HAA  
 GGCCTTAAGCCGCGTCCGCGNNNN-----N  
 3' end for 7 VII genes: DP31, DP33, DP39, DP40, DP47 and DP49  
 CCGGAATTTCGCGCCAGCGCCNNNN-----NCA  
 GGCCTTAAGCCGCGTCCGCGNNNN-----N  
 3' end for 4 VII genes: DP2, DP3, DP5 and DP38

All kappa genes:  
 Asp Pro  
 NNN-----CCT  
 GGNNN-----G  
 (except VK L20)

JK1 gene / NotI / PCR primer site /  
 TrpThrPheGlyGlnGlyThrLysValGluLeuLys  
 TCGACGTTTCGCGCCAGCGCCNNNN-----HAA  
 GAACCTCCAGCGCGTCCCTCGTCCACCTTTAGTTTCGCGCGGTCCACCTCAGCTCAGTTT

JK2 gene /  
 TyrThrPheGlyGlnGlyThrLysValGluLeuLys  
 TACACTTTTCGCGCCAGCGCCNNNN-----HAA  
 GAATGTCAGAACCGCGTCCCTCGTCCACCTCAGTTT

JK3 gene /  
 PheThrPheGlyProGlyThrLysValAspLeuLys  
 TTCACCTTTTCGCGCCAGCGCCNNNN-----HAA  
 GAAAGTCAGAACCGCGTCCCTCGTCCACCTCAGTTT

DPL16 (=v3s1)+  
 Lambda 3 genes: / +v318 /  
 Ser His  
 NNN-----CAT  
 GGNNN-----G  
 for DPL16+V318 / NotI / PCR primer site /  
 ValValPheGlyGlyThrLysLeuThrValLeu  
 GTGGTATTCGCGCGGAGGACCAAGCTGACCGTCTAGCGCGCGCGCAGTGTGAGTCCAAAAGATTTTCG  
 TACACCATAGCCCGCTCCCTCGTTCGACTGGCAGGATCCGCGCGGTCCACACTCAGCTCAGTTTCTAAAGC

Lambda 3 gene: /DPL23 (=VL3.11)/  
 Ser Ala  
 NNN-----GCA  
 GGNNN-----C  
 for DPL23+VL3.1  
 GTG--- continued as for JL2/3  
 GTCAC---

Lambda 1 genes: / DPL2+DPL3 /  
 Gln Gly  
 NNN-----GGT  
 GGNNN-----C  
 for DPL2+DPL3  
 GTG--- continued as for JL2/3  
 CACAC---

Lambda 2 gene: / DPL11 /  
 Gln Leu  
 NNN-----CTC  
 GGNNN-----G  
 for DPL11  
 GTG--- continued as for JL2/3  
 AGCAC---

FIGURE 33

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCCG	CCATGGCCCA	GGTGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTAAAGCCT	60
	Q	V Q L	V E S G	G G L	V K P	
GGGGGICCC	TTAGACTCTC	CTGTGCAGCC	TCGTGATTC	CTTTCAGTAA	CGCCTGGATG	120
G G S L	R L S	C A A	S G F T	F S N	A W M	
AGCTGGGTCC	GCCAGGCTCC	AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAAGCAAA	180
S W V R	Q A P	G K G	L E W V	G R I	K S K	
ACTGATGGTG	GGACAACAGA	CTACGCTGCA	CCCGTGAAG	GCAGATTCAC	CATCTCAAGA	240
T D G G	T T D	Y A A	P V K G	R F T	I S R	
GATGATTCAA	AAAACACGCT	GTATCTGCAA	ATGAACAGCC	TGAAAACCGA	GGACACAGCC	300
D D S K	N T L	Y L Q	M N S L	K T E	D T A	
GTTTATTACT	GTACCACAGT	TGCGTTGTCT	GCCGACCGTG	GGATGTGGGG	TCAAGGAACT	360
V Y Y C	T T V	A L S	A D R G	M W G	Q G T	
CTGGTCACCG	TCTCTCAGG	TGGAGGCGGT	TCAGGCGGAG	GTGGCTCTGG	CGGTGGCGGA	420
L V T V	S S G	G G G	S G G G	G S G	G G G	
TCCGATGTTG	TGATGACTCA	GTCTCCACTC	TCCCTGCCCC	TCACCCCTTG	ACAGCCCGCC	480
S D V V	M T Q	S P L	S L P V	T L G	Q P A	
TCCATCTCCT	GCAGGTCTAG	TCAAAGCCTC	GTATACAGTG	ATGGAAACAC	CTACTTGAAT	540
S I S C	R S S	Q S L	V Y S D	G N T	Y L N	
TGGTTTCAGC	AGAGGCCAGG	CCAATCTCCA	AGGCGCCTAA	TTTATAAGGT	TTCTAACCGG	600
W F Q Q	R P G	Q S P	R R L I	Y K V	S N R	
GACTCTGGGG	TCCCAGACAG	ATTGAGCGGC	AGTGGGTCAG	GCACTGATTT	CACACTGAAA	660
D S G V	P D R	F S G	S G S G	T D F	T L K	
ATCAGCAAGG	TGGAGGCTGA	GGATGTTGGG	GTTTATTACT	GCATGCAAGG	TACACACTGG	720
I S R V	E A E	D V G	V Y Y C	M Q G	T H W	
CCTTACACTT	TTGGCCAGGG	GACCAAGCTG	GAGATCAAAG	CGGCGGC		767
P Y T F	G Q G	T K L	E I K			

FIGURE 34

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGGCCGG	CCATGGCCCA	GATGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTAAAGCCT	60
	Q	M Q L	V E S G	G G L	V K P	
GGGGGGTCCC	TTAGACTCTC	CTGTGCAGCC	TCCTGATTC	CITTCAGTAA	CGCCTGGATG	120
G G S L	R L S	C A A	S G F T	F S N	A W M	
AGCTGGGTCC	GCCAGGCTCC	AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAAGCAAA	180
S W V R	Q A P	G K G	L E W V	G R I	K S K	
ACTGATGGTG	GGACACAGA	CTACGCTGCA	CCCGTGAAG	GCAGATTAC	CATCTCAAGA	240
T D G G	T T D	Y A A	P V K G	R F T	I S R	
GATGATTCAA	AAAACACGCT	GATCTTGCAA	ATGAACAGCC	TGAAAACCGA	GGACACAGCC	300
D D S K	N T L	Y L Q	M N S L	K T E	D T A	
GTGTATTACT	GTACCACATG	GGGTCCTGTC	GACACGGACA	ACTACGCCAG	GTTTTGGGGT	360
V Y Y C	T T W	G S V	D T D N	Y A R	F W G	
CAAGGAATCT	TGGTCACCGT	CTCTCAGGT	GGAGGCGGTT	CAGGCGGAGG	TGGCTCTGGC	420
Q G T L	V T V	S S G	G G G S	G G G	G S G	
GGTGGCGGAT	CCGACATCCA	GATGACCCAG	TCTCCATCCT	CCCTGTCTGC	ATCTGTAGGA	480
G G G S	D I Q	M T Q	S P S S	L S A	S V G	
GACAGAGTCA	CCATCACTTG	CCGGGCGAGT	CAAGGCATTA	GCAATTATTT	AGCCTGGTAT	540
D R V T	I T C	R A S	Q G I S	N Y L	A W Y	
CAGCAGAAC	CAGGGAAAGT	TCCTAAGCTC	CTGATCTATG	CTGCATCCAC	TTTGCAATCA	600
Q Q K P	G K V	P K L	L I Y A	A S T	L Q S	
GGGGTCCCAT	CTCGGTTTCAG	TGGCAGTGG	TCTGGGACAG	ATTTCACTCT	CACCATCAGC	660
G V P S	R F S	G S G	S G T D	F T L	T I S	
AGCCTGCAGC	CTGAAGATGT	TGCAACTTAT	TACTGTCAAA	AGTATAACAG	TGCCCCCTCTC	720
S L Q P	E D V	A T Y	Y C Q K	Y N S	A P L	
ACTTTCCGGC	GAGGGACCAA	GGTGGAGATC	AAAGCGGCGC			761
T F G G	G T K	V E I	K			

4

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCCG	CCATGGCCCA	GATGCAGCTG	GTTGAGTCTG	GGGGAGGCTT	GGTAAAGCCT	60
	Q	M Q L	V E S G	G G L	V K P	
GGGGGGTCCC	TTAGACTCTC	CTGTGCAGCC	TCTGGATTCA	CTTTCAGTAA	CGCCTGGATG	120
G G S L	R L S	C A A	S G F T	F S N	A W M	
AGCTGGGTCC	GCCAGGCTCC	AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAAGCAAA	180
S W V R	Q A P	G K G	L E W V	G R I	K S K	
ACTGATGGTG	GGACACAGA	CTACGCTGCA	CCCGTGAAAG	GCAGATTAC	CATCTCAAGA	240
T D G G	T T D	Y A A	P V K G	R F T	I S R	
GATGATTCAA	AAAACACGCT	GATCTGCAA	ATGAACAGCC	TGAAAACCGA	GGACACAGCC	300
D D S K	N T L	Y L Q	M N S L	K T E	D T A	
GTGTATTACT	GTAACACACC	GGGCTGGTAT	GGGGCCGAGG	ATAAGTGGGG	TCAAGGAACT	360
V Y Y C	T T P	G W Y	G A E D	K W G	Q G T	
CTGGTCACCG	TCTCTCAGG	TGGAGGGGGT	TCAGGGGGAG	GTGGCTCTGG	CGGTGGGGGA	420
L V T V	S S G	G G G	S G G G	G S G	G G G	
TCCGACATCC	AGATGACCCA	GTCCTCATCC	TCCCTGTCTG	CATCTGTAGG	AGACAGAGTC	480
S D I Q	M T Q	S P S	S L S A	S V G	D R V	
ACCATCACTT	GCCGGGGGAG	TCAGGGCATT	AGCAATTATT	TAGCCTGGTA	TCAGCAGAAA	540
T I T C	R A S	Q G I	S N Y L	A W Y	Q Q K	
CCAGGGGAAG	TTCTTAAGCT	CCTGATCTAT	GCTGCATCCA	CTTTGCAATC	AGGGGTCCCA	600
P G K V	P K L	L I Y	A A S T	L Q S	G V P	
TCTCGGTTCA	GTGGCAGTGG	ATCTGGGACA	GATTTCACTC	TCACCATCAG	CAGCCTGCAG	660
S R F S	G S G	S G T	D F T L	T I S	S L Q	
CCTGAAGATG	TTGCAACTTA	TTACTGTCAA	AAGTATAACA	GTGCCCCCTT	CACCTTTCGGC	720
P E D V	A T Y	Y C Q	K Y N S	A P F	T F G	
CCTGGGACCA	AAGTGGATAT	CAAAGCGGCC	GC			752
P G T K	V D I K					

1

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

29

30

31

32

33

34

35

36

37

38

39

40

41

42

43

44

45

46

47

48

49

50

51

52

53

54

55

56

57

58

59

60

61

62

63

64

65

66

67

68

69

70

71

72

73

74

75

76

77

78

79

80

81

82

83

84

85

86

87

88

89

90

91

92

93

94

95

96

97

98

99

100

101

102

103

104

105

106

107

108

109

110

111

112

113

114

115

116

117

118

119

120

121

122

123

124

125

126

127

128

129

130

131

132

133

134

135

136

137

138

139

140

141

142

143

144

145

146

147

148

149

150

151

152

153

154

155

156

157

158

159

160

161

162

163

164

165

166

167

168

169

170

171

172

173

174

175

176

177

178

179

180

181

182

183

184

185

186

187

188

189

190

191

192

193

194

195

196

197

198

199

200

201

202

203

204

205

206

207

208

209

210

211

212

213

214

215

216

217

218

219

220

221

222

223

224

225

226

227

228

229

230

231

232

233

234

235

236

237

238

239

240

241

242

243

244

245

246

247

248

249

250

251

252

253

254

255

256

257

258

259

260

261

262

263

264

265

266

267

268

269

270

271

272

273

274

275

276

277

278

279

280

281

282

283

284

285

286

287

288

289

290

291

292

293

294

295

296

297

298

299

300

301

302

303

304

305

306

307

308

309

310

311

312

313

314

315

316

317

318

319

320

321

322

323

324

325

326

327

328

329

330

331

332

333

334

335

336

337

338

339

340

341

342

343

344

345

346

347

348

349

350

351

352

353

354

355

356

357

358

359

360

361

362

363

364

365

366

367

368

369

370

371

372

373

374

375

376

377

378

379

380

381

382

383

384

385

386

387

388

389

390

391

392

393

394

395

396

397

398

399

400

401

402

403

404

405

406

407

408

409

410

411

412

413

414

415

416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

431

432

433

434

435

436

437

438

439

440

441

442

443

444

445

446

447

448

449

450

451

452

453

454

455

456

457

458

459

460

461

462

463

464

465

466

467

468

469

470

471

472

473

474

475

476

477

478

479

480

481

482

483

484

485

486

487

488

489

490

491

492

493

494

495

496

497

498

499

500

501

502

503

504

505

506

507

508

509

510

511

512

513

514

515

516

517

518

519

520

521

522

523

524

525

52

10	20	30	40	50	60
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GGCCAGGCGG	CCATGGCCCA	GGTGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTACAGCCT
	Q	V Q L	V E S G	G G L	V Q P
GGGGATTCUC	TGAGACTCTC	CTGTGCAGCC	TCTGGATTC A	CCCTTCAGTAA	CAGTGACATG
G G S L	R L S	C A A	S G F T	F S N	S D M
AACTGGGTCC	ATCAGGCTCC	AGGAAGGGG	CTGGAGTGGG	TATCGGGTGT	TAGTTGGAAT
N W V H	Q A P	G K G	L E W V	S G V	S W N
GGCAGTAGGA	CGCACTATGC	AGACTCTGTG	AAGGGCCGAT	TCATCATCTC	CAGAGACAAT
G S R T	H Y A	D S V	K G R F	I I S	R D N
TCCAGGAACA	CCCTGTATCT	GCAACGAAT	AGCCTGAGGG	CCGAGGACAC	GGCTGTGTAT
S R N T	L Y L	Q T N	S L R A	E D T	A V Y
TACTGTGTGA	GACCCGATGG	CGAGTGGTAC	GGGGCCTGGG	GTCAAGGAAC	TCTGGTCACC
Y C V R	T D G	E W Y	G A W G	Q G T	L V T
GTCTCCTCAG	GTGGAGGGGG	TTCAGGGCGA	GGTGGCTCTG	GGGGTGCGGG	ATCCGGCATT
V S S G	G G G	S G G	G G S G	G G G	S A I
CAGATGACCC	AGTCTCCATC	CTCCCTGTCT	GCATCTGTAG	GAGACAGAGT	CACCATCACT
Q M T Q	S P S	S L S	A S V G	D R V	T I T
TGCCGGGGCA	GTGAGGGCAT	TAGAATGAT	TTAGGCTGGT	ATCAGCAGAA	ACCAGGGAAA
C R A S	Q G I	R N D	L G W Y	Q Q K	P G K
GGCCCTAAGC	TCCGGATCTA	TGCTGCATCC	AGTTTACAAA	GTGGGGTCCC	ATCAAGGTTT
A P K L	R I Y	A A S	S L Q S	G V P	S R F
AGCGGCAGTG	GATCTGGCAC	AGATTTCACT	CTCACCATCA	GCAGCCTGCA	GCTGAAGAT
S G S G	S G T	D F T	L T I S	S L Q	P E D
TTTGCAACTT	ATTACTGTCT	ACAAGATTAC	AATTACCTTC	TCACTTTGGG	CGGAGGGACC
F A T Y	Y C L	Q D Y	N Y P L	T F G	G G T
AAGGTGGAGA	TCAAAGCGGC	CGC			
K V E I K					

FIGURE 37







006200 3000000

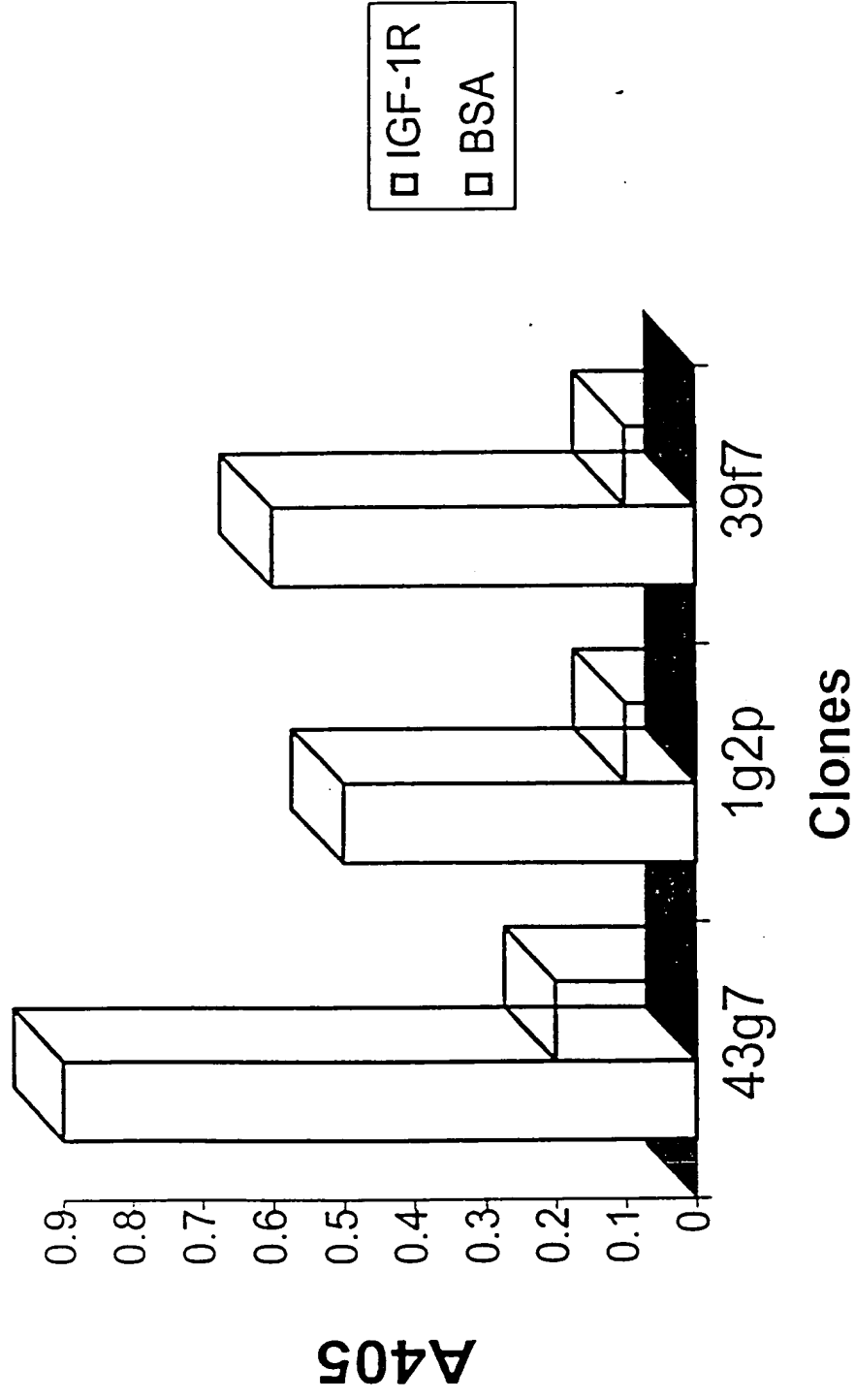


FIGURE 40

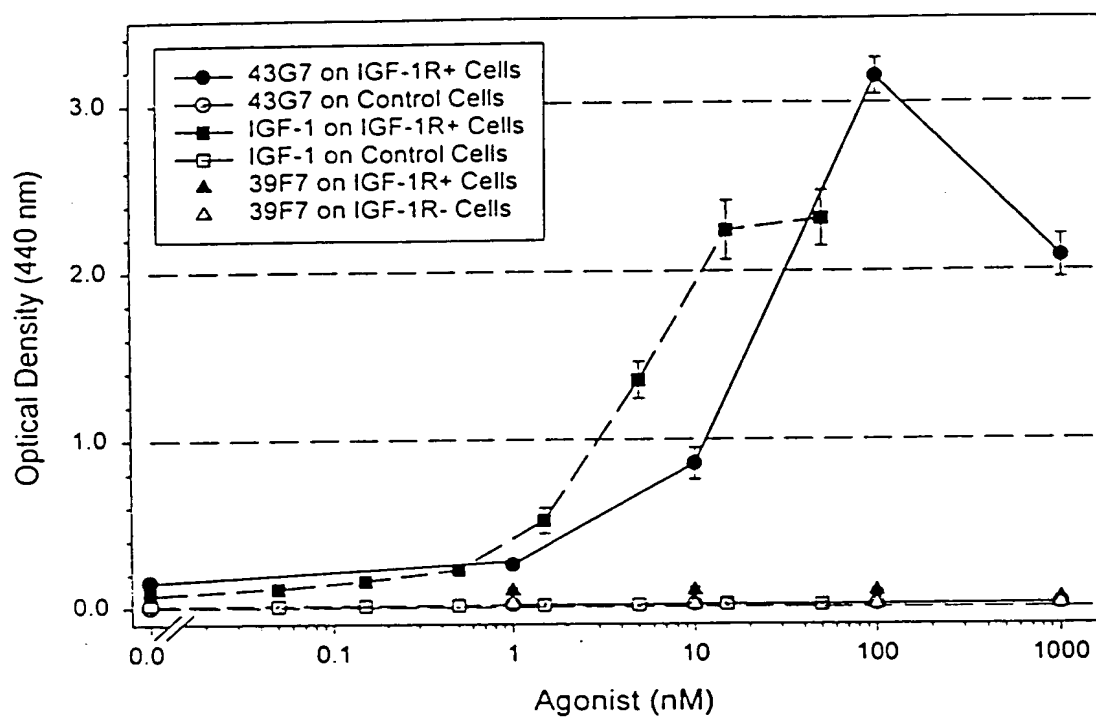


FIGURE 41

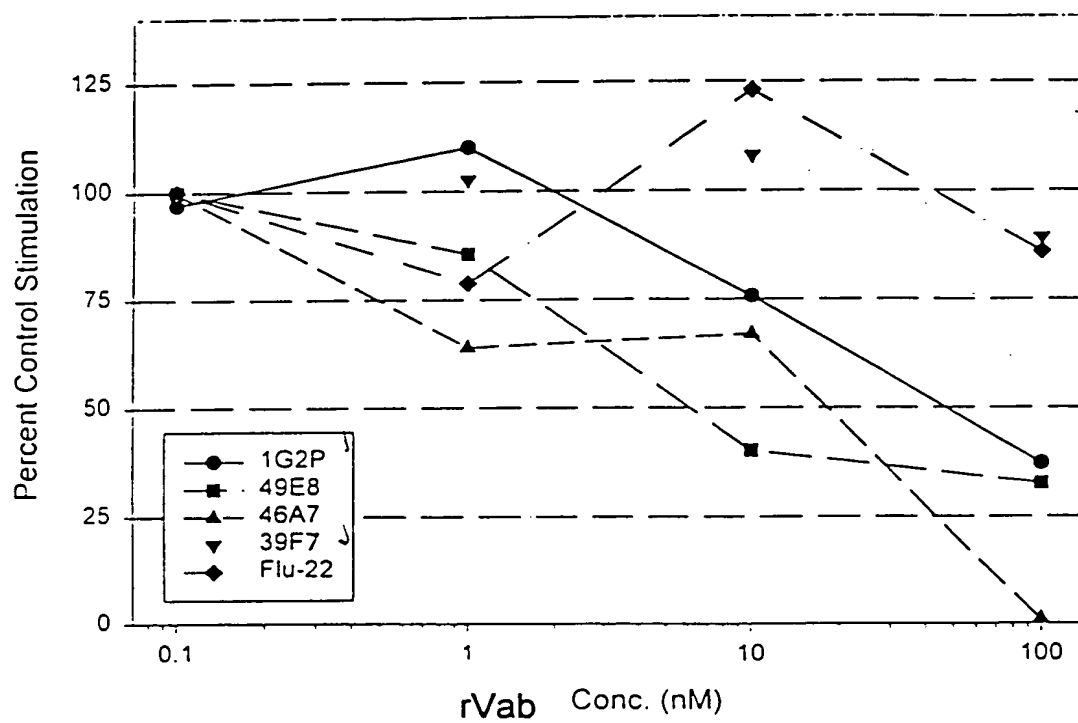


FIGURE 42

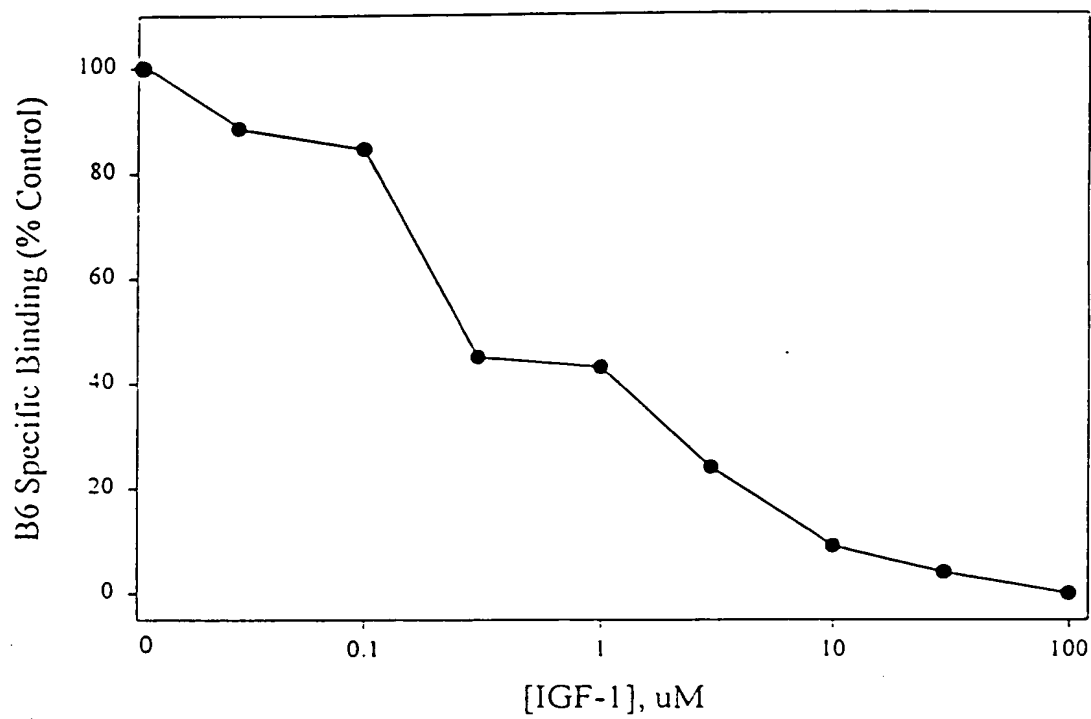


FIGURE 43

rVab 43G7 Specific Binding (% Control)



FIGURE 44

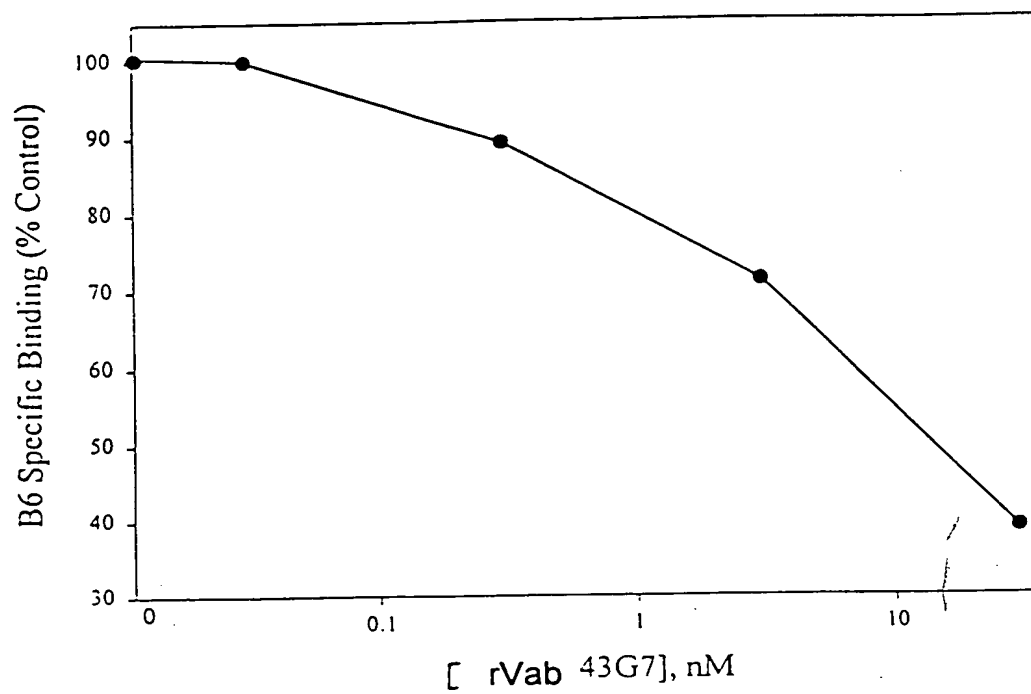


FIGURE 45



FIGURE 46A

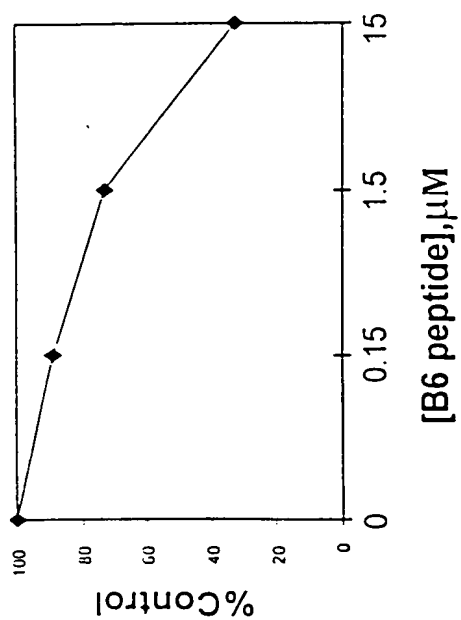


FIGURE 46B

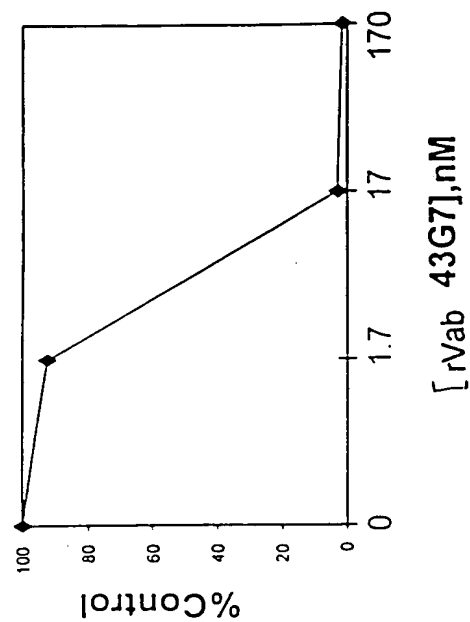


FIGURE 46C

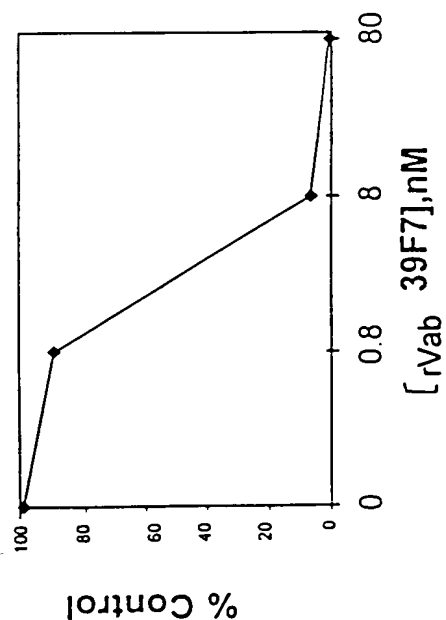
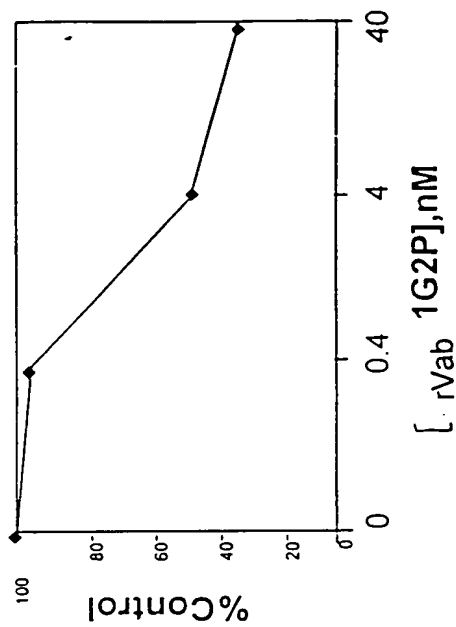


FIGURE 46D



Group 1: Formula 1 Motif

		Target	
		Found	IR
20D3*	IGGGQHGDGNEFYDWFVEALA	18	+
20F1	VFWNCRSQQLDEFYEFQAA	16	+
G3	RGGTFFYEFESALRKHGAG	8	+
20H1	RVAGAISAPGLVSNKQDGLFYSWRE	5	+
20D1*	VLQARIIGCDSDCFYEWFA	4	+
D2	DPERMQSDVGFYEFTRAAG	3	+
B8	WSALLSVMDTGFYAWEDDAV	2	++
C4	DIGSDGHGRRWDSFYRWFEEM	2	+
A8	IGGSFVEFYGWENDQV	2	+
E7	GHSWALVRHVDRRLFYEWFDL	1	++
C8	LPAGGAQGFVVRGFYEFES	1	+
H8	RDKPTDQEEQNWSFYEFERH	1	+
E2	SRDQTNFTFNSAGFYGWFER	1	+
B12	GNFYRWTFHEALVGSERVPDV	1	+
D10-2	RIGGGWARSEGFYEFVREL	1	+
G8	RMFYEFWSQMGAGPTEGSA	1	+
I13	HEAFYDWFSAALVDGGYELMG	1	+
3G11	FYGFWSRQLSLTPRDDWGLP	1	+
F4	GVGTLTMSSDAFYTWEV	1	+
E7-2	LGTSAGQGVGHRAFYQWFQS	1	+
40G11	-----AALDRLFYSWFS	3	+
40R2	<--ETLESHYVVTQ-----	2	+
40B12	IRDMHYVWVQDRDRYINCVRQWYISDRYNPGSAFYRWFD	1	+
	RMGLQALAHYRKSA-----GPIFLSSGSVIKGSEGDPFYAWFRLQ	1	+

FIGURE 47

**Group 2: Formula 6 Motif**

20A4\* EIEAEWGRVRCIVYGRCVGG  
DS WLDQEWANWOCFVYGRGCP

Target	
Found	IR IGF
13	+++ 0
3	+++ ?

**Group 3: Formula 2 Motif**

20E2 DYKDFYDAIDQLVRGSARAGTRD  
20C11 DYKDDRAFYNGLRDLVGAVYGAWD  
20A12 DYKDRIFYCGIQALGANLGYSGCV  
C6 DYKDFYSALWGLCGVTGCG  
A6 RGQSDAFYSGGLWALIGLSDG

Target	
Found	IR IGF
1	+ +++++
1	+ +++++
1	+ +++++
1	+ +++++
1	+ +++++

**Group 5: Miscellaneous Motif 10**

D0.2 PFGGGRWNGIPRWYRNS  
114 WWWGGRNRWWLFRWGLGGER

Target	
Found	IR IGF
1	++ ++
1	+ +

**Group 4 and 6: Miscellaneous Motif 10**

D10 LGPLLRWGSSEVCGVWPDCE  
F2 SMFVAGSDRWPGYGVLDWL  
F8 VRGFQGGTVWPGYEWLRNAA  
A2 CRVALNGFVWPRWMSRPV  
A4 WPGYLEFEALQDWRGSTD

Target	
Found	IR IGF
3	++ 0
1	++ ++
1	++ ?
1	++ +
1	0 +++

**Group 7: Formula 4 Motif**

F8 HLCVLEELFWGASLFGYCSG  
B6 ACSSEFVKPGEGLQCLGSI  
40D6 PERGRCLRTAMQIMRRPRDWWIIFPHSLFWGAPPLSG

Target	
Found	IR IGF
4	+++ +
1	0 ++
1	0 0

**Group 8: Non-Aligning  
Miscellaneous  
Sequences**

FIGURE 49A

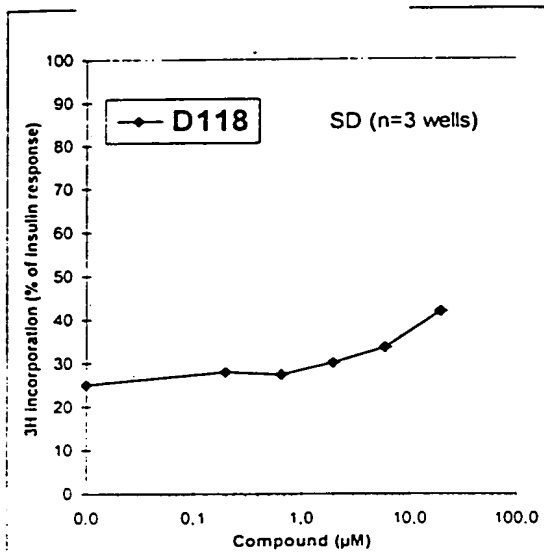


FIGURE 49B

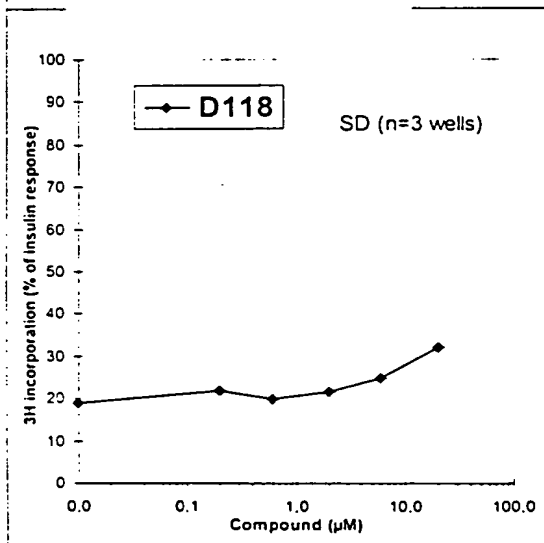
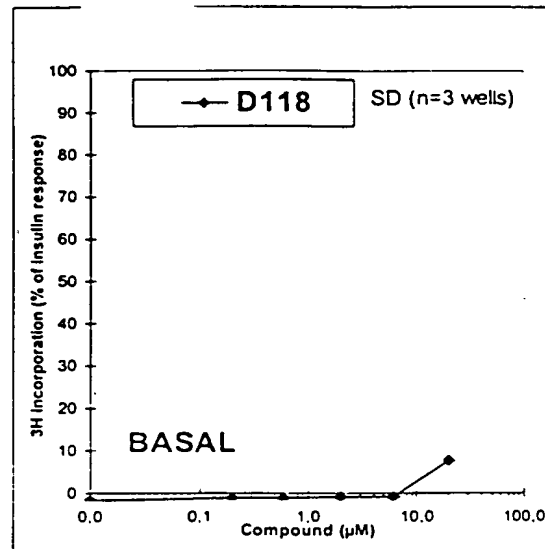


FIGURE 49C

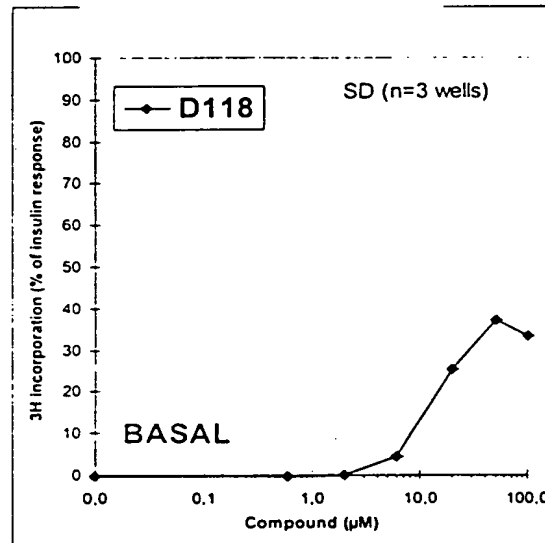


FIGURE 49D

FIGURE 50A

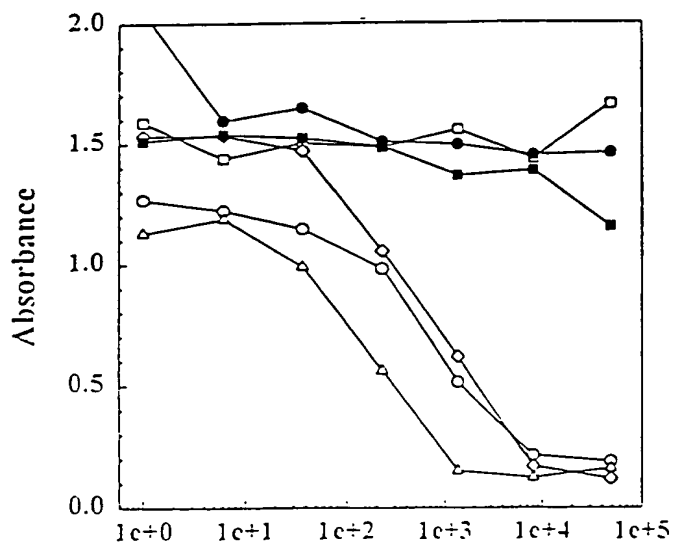


FIGURE 50B

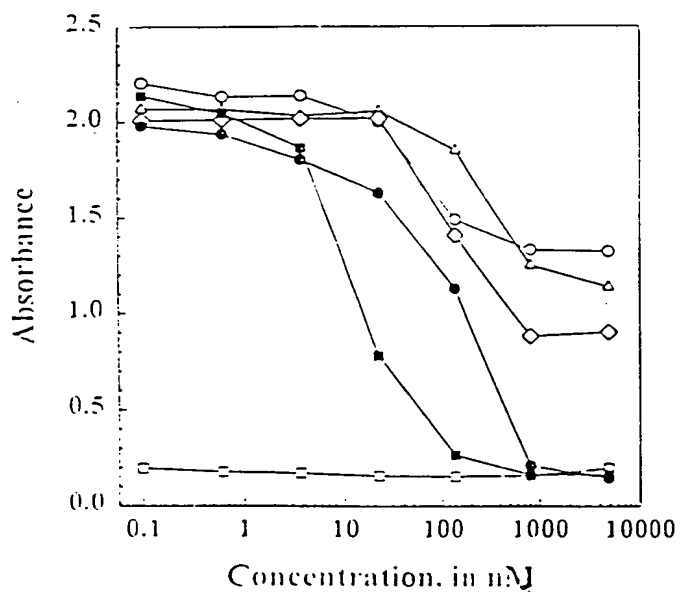
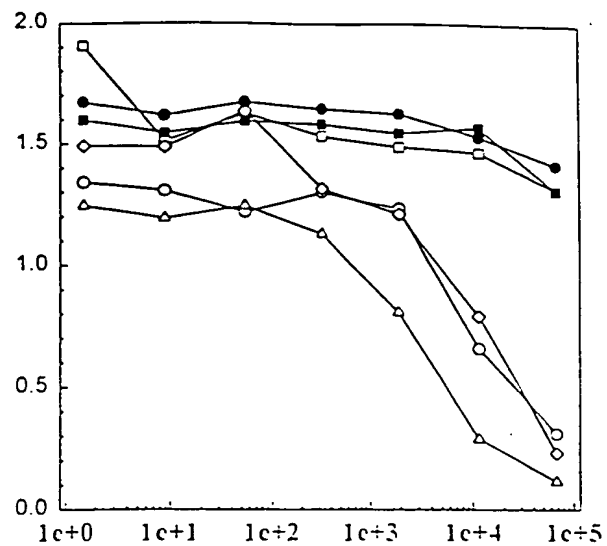


FIGURE 50C

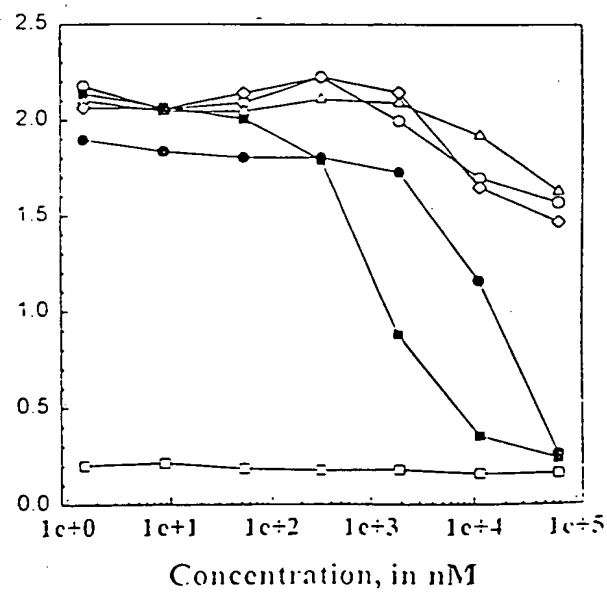


FIGURE 50D

FIGURE 51A

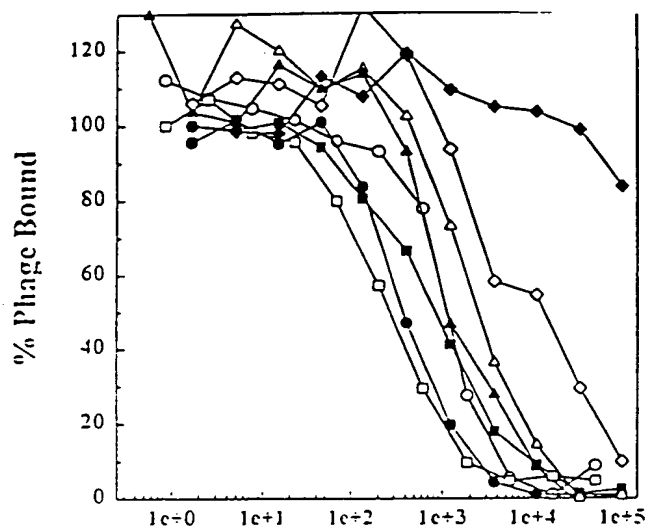


FIGURE 51B

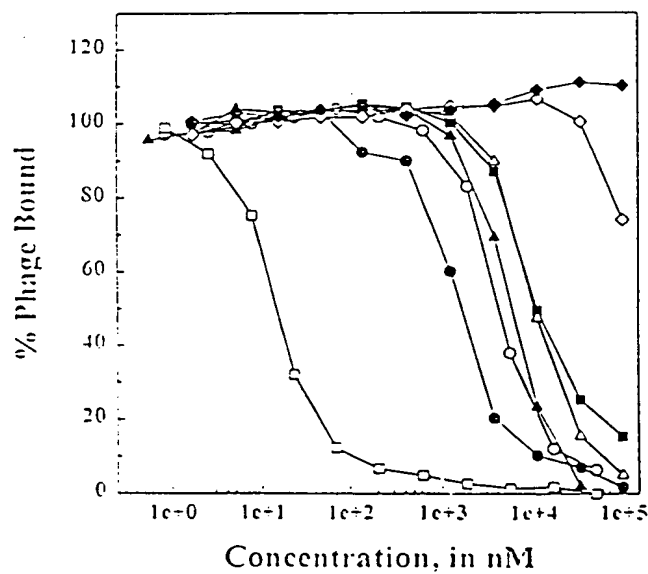
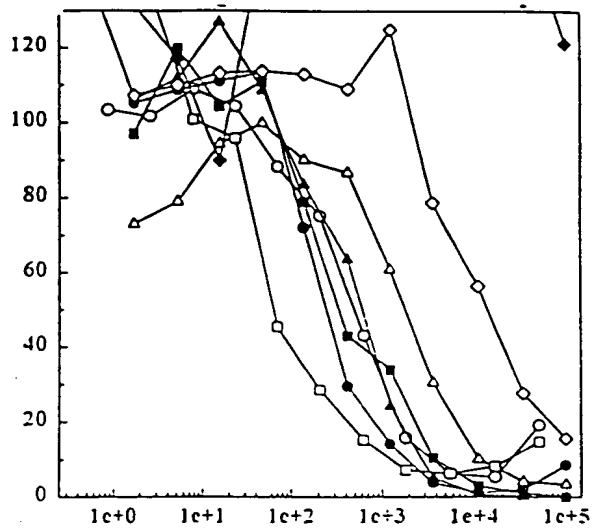


FIGURE 51C

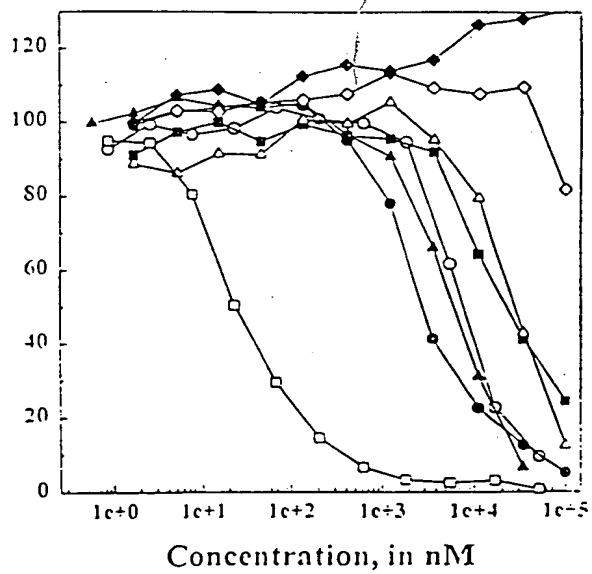


FIGURE 51D

FIGURE 52A

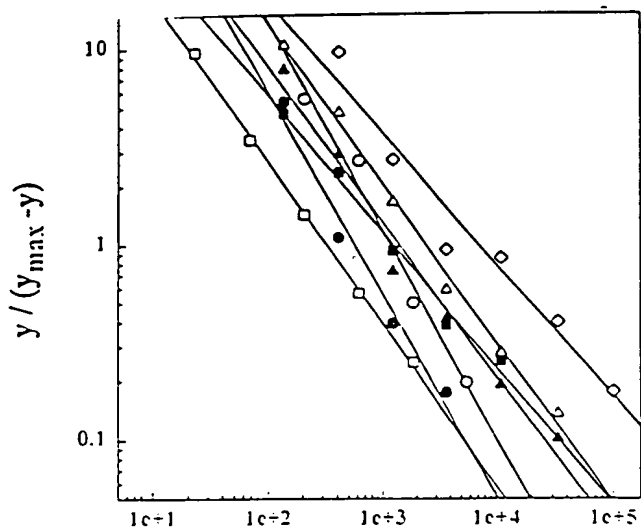


FIGURE 52B

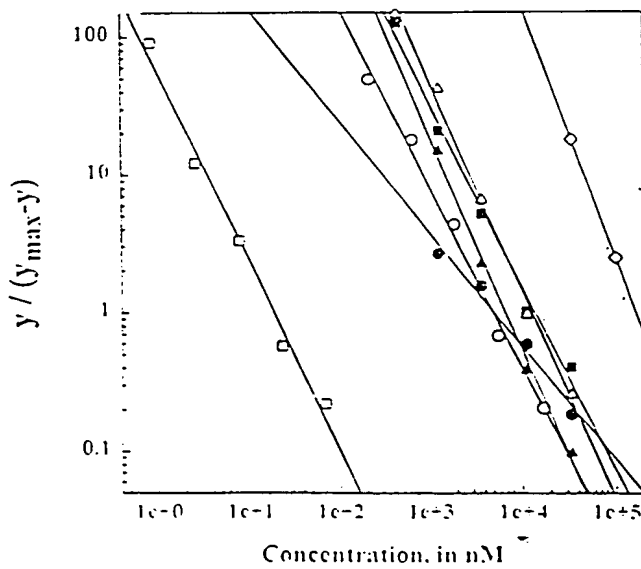
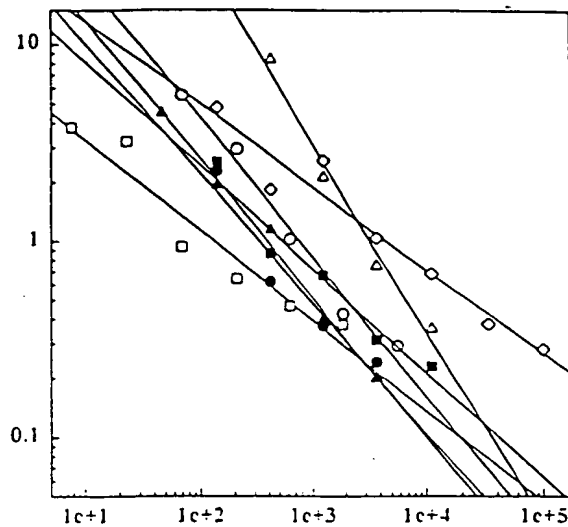


FIGURE 52C

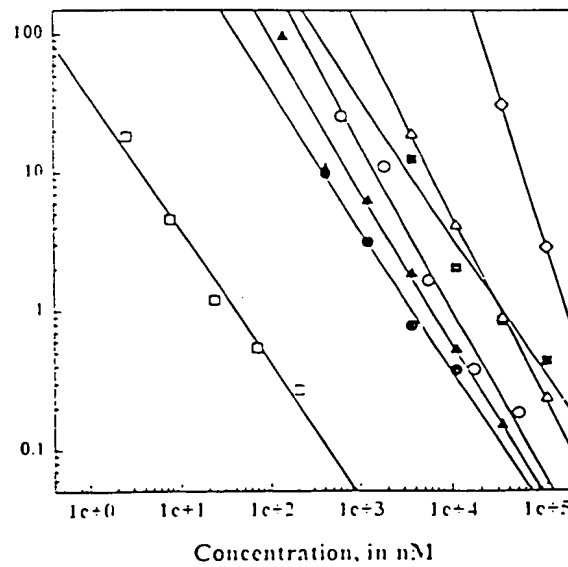


FIGURE 52D







011453671 20030606

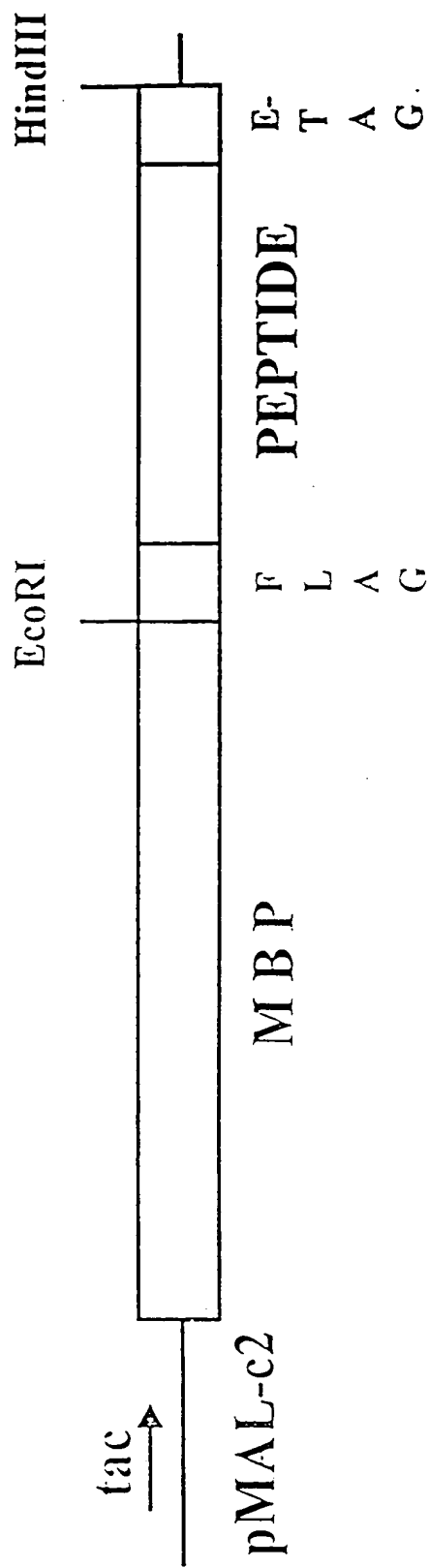


FIGURE 55

Normalized Phage Signal, % Control

FIGURE 56A

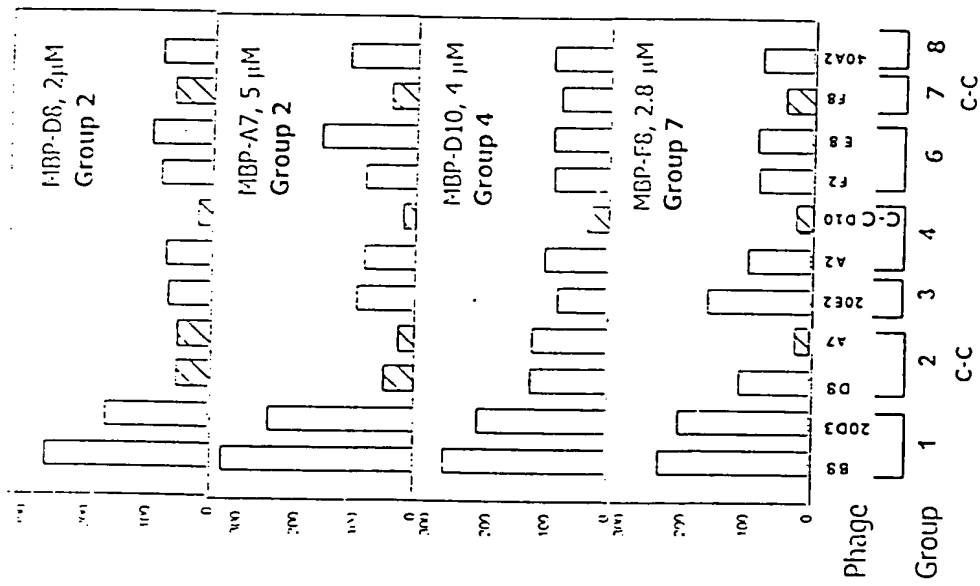


FIGURE 56B

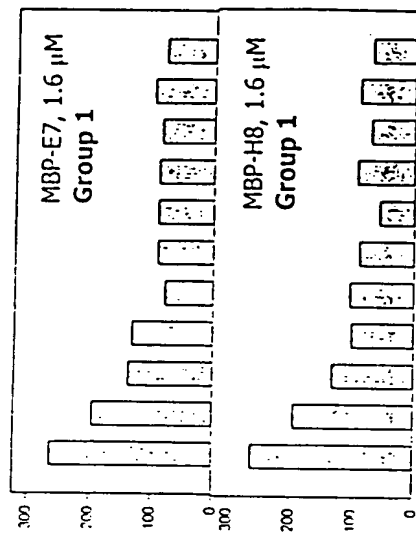
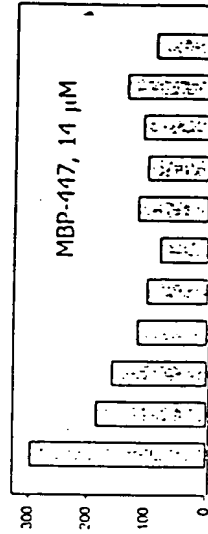


FIGURE 56C



10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GCCCAGCCCG	CCATGGCCGA	GGTGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTAAAGCCT	60
	E	V	Q	L	V	E
		S	G	G	L	V
						K
						P
GGGGGGTCCC	TTAGACTCTC	CTGTGCAGCC	TCTGGATTCA	CTTTCAGTAA	CGCTCGGATG	120
G	G	S	L	R	L	S
		C	A	A	S	G
			F	T	F	S
					N	A
						W
						M
AGCTGGGTCC	GCCAGGCTCC	AGGGAAGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAGCGAA	180
S	W	V	R	Q	A	P
		G	K	G	L	E
			W	V	G	R
					I	K
						S
						K
ACTGATGGTG	GGACAACAGA	CTACGCTGCA	CCCGTGAAG	GCAGATTCAC	CATCTCAAGA	240
T	D	G	G	T	T	D
		Y	A	A	P	V
			K	G	R	F
					T	I
						S
						R
GATGATTCAA	AAACACGGT	GTATCTGCA	ATGACAGCC	TGAAACCGA	GGACACAGCC	300
D	D	S	K	N	T	L
		Y	L	Q	M	N
			S	L	K	T
					E	D
						T
						A
GCTATTACT	GTACCACATA	CGGCGACGTT	TACGACCGCG	ATTACGATGG	GCGTGGGGT	360
V	Y	Y	C	T	T	Y
		G	D	V	Y	D
			R	D	Y	D
					G	R
						W
						G
CAAGGACTC	TGGTCAOCT	CTCTCAGT	GGAGGGGTT	CAAGGGAGG	TGGCTCTGGC	420
Q	G	T	L	V	T	V
		S	S	G	G	G
			S	G	G	G
					G	S
						G
						/
GGTGGGGT	CCGACATCA	GATGACCA	TCTCATCT	CCCTGCTCG	ATCTGTAG	480
G	G	G	S	D	I	Q
		M	T	Q	S	P
			S	S	L	S
					A	S
						V
						G
GACGAGTCA	CCATCACTTG	CGGGGAGT	CAAGGATTA	GCATTATTT	AGCTGGTAT	540
D	R	V	T	I	T	C
		R	A	S	Q	G
			I	S	N	Y
					L	A
						W
						Y
CAAGGAAAC	CAAGGAAAT	TCTTAGGTC	CTGATCTATG	CTGATCCAC	TTTGATCA	600
Q	Q	K	P	G	K	V
		P	K	L	L	I
			Y	A	A	S
					T	L
						Q
						S
GGGTCCCT	CTGGTTCAG	TGGGATGGA	TCTGGGAGG	ATTTCATCT	CACTTCAGT	660
G	V	P	S	R	F	S
		G	S	G	S	G
			T	D	F	T
					L	T
						I
						S
AGCTGCAAG	CTGAGATGT	TGCACTTAT	TACTGTGAA	ASTATAACAG	TGCCCCTTTC	720
S	L	Q	P	E	D	V
		A	T	Y	Y	C
			Q	K	Y	N
				S	A	P
						F
ACTTTCGACC	CTGGAACAA	AGTGTATTC	AAAACGGCCG	C		761
T	F	G	P	G	T	K
		V	D	I	K	

FIGURE 57



	CLONES	VHCDR3	%Inhibition Activity
	118:	PFFV	FYRGQDT 54%
?	InsulB:	FVNQHLCGSHLV <del>EA</del> LY LV <del>CG</del> RG <del>F</del> YTPKT	
	12H10:	C VVYNYA G RG T	42%
Ang?	13-e-4:	VQANDGL G RES	52%
?	13h9:	GGL G RRDWL	30%
?	24:	GGRR H RLG	
	InsulinA	GIVEQCCTSI <del>C</del> SLYQ <u>LENYCN</u>	
	11a8:	ENYGNSE	32%
?		GDQELQNY	None
	N/A		

FIGURE 59

Figure 1 is a line graph showing the effect of concentration on A440nm absorbance. The x-axis represents A440nm (0 to 2) and the y-axis represents Concentration [nM] (0.1 to 1000). Three data series are plotted: open circles (○), solid circles (●), and open squares (□). The open circle series shows a sharp increase in absorbance at high concentrations, while the solid circle series shows a moderate increase. The open square series shows a sharp increase in absorbance at high concentrations, similar to the open circle series.

Concentration [nM]	A440nm (○)	A440nm (●)	A440nm (□)
0.1	0.05	0.05	0.05
1	0.15	0.15	0.15
10	0.55	0.55	0.55
100	1.55	1.15	1.15
1000	1.95	1.55	1.55

FIGURE 60

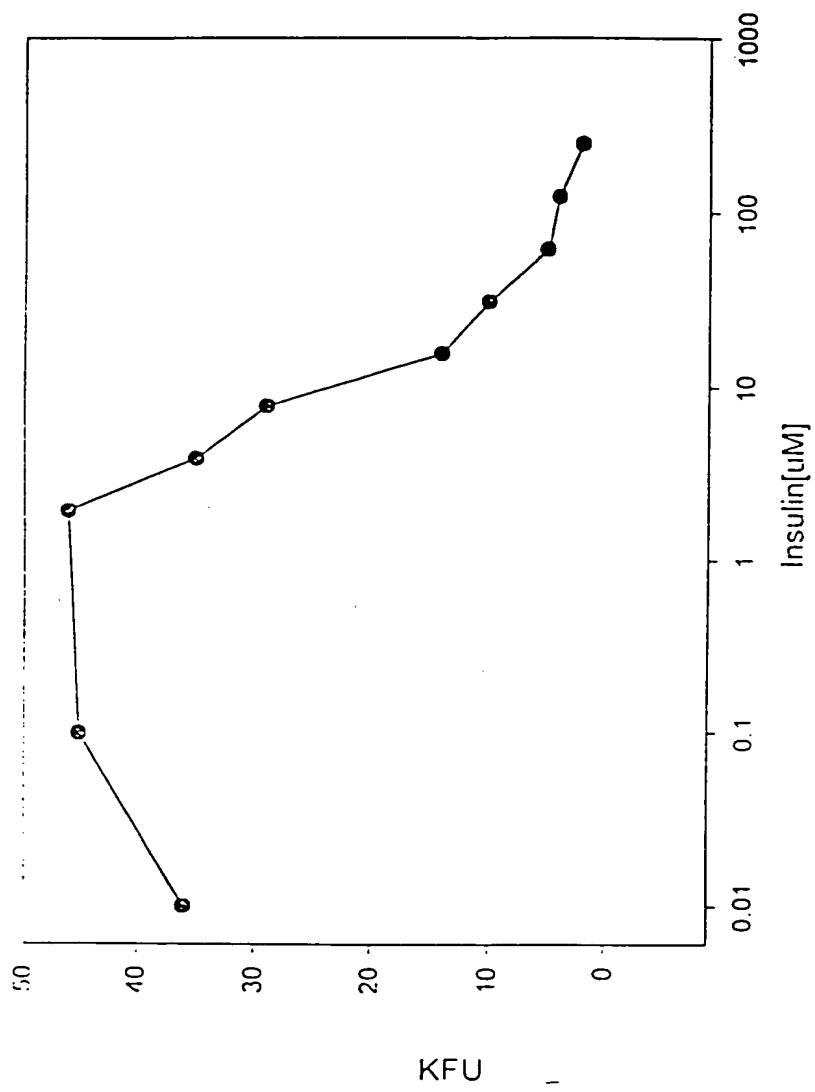


FIGURE 61





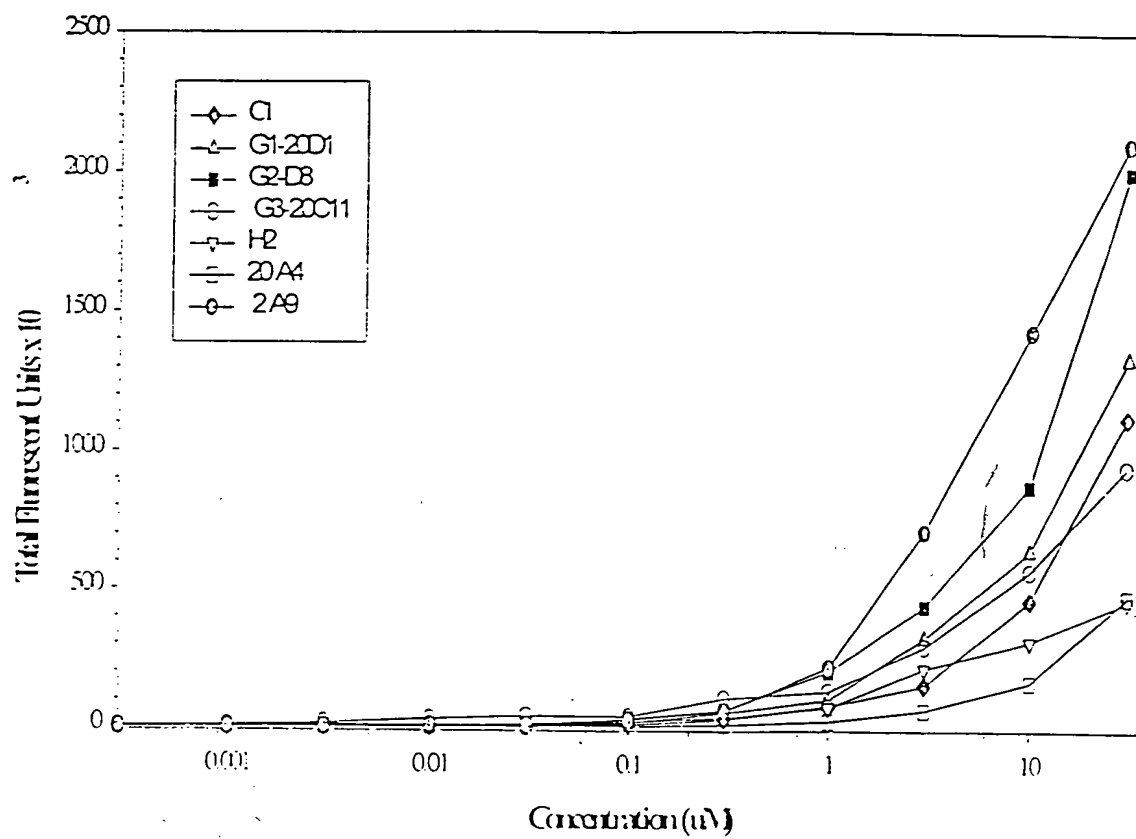
[illegible]

FIGURE 63

Figure 1 is a log-log plot showing the binding of  $^{125}\text{I}$ -IGF-I to IGF-1R and IGF-2R. The y-axis represents 'Fluorescent Units  $\times 10^3$ ' (0 to 2000) and the x-axis represents 'Concentration (nM)' (1e-2 to 1e6). The plot includes six data series as defined in the legend:

- C1 (IGFR) T (open circles)
- +IGF (IGFR) B (open squares)
- Specific (IGFR) (filled triangles)
- C1 (IR) T (open inverted triangles)
- +IGF (IR) B (open circles)
- Specific (IR) (open diamonds)

The IGFR binding (C1, +IGF, Specific) shows a peak around 1e+1 nM. The IR binding (C1, +IGF, Specific) shows a sharp increase starting around 1e+4 nM.

FIGURE 64

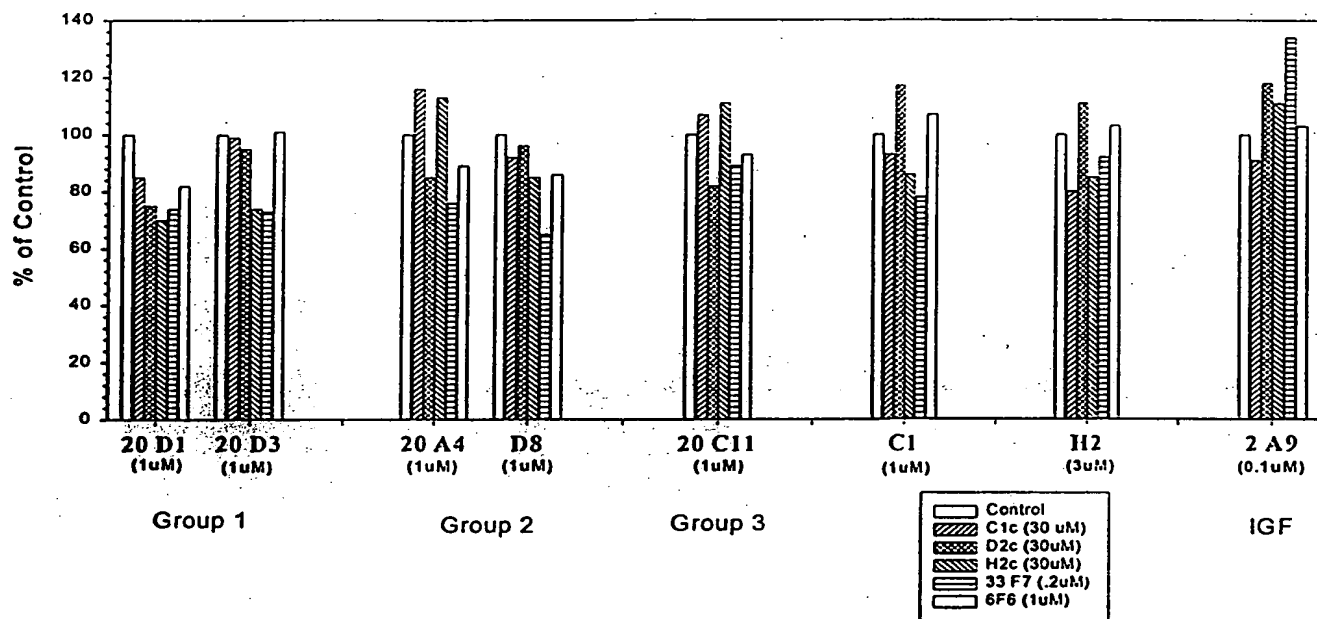


FIGURE 65

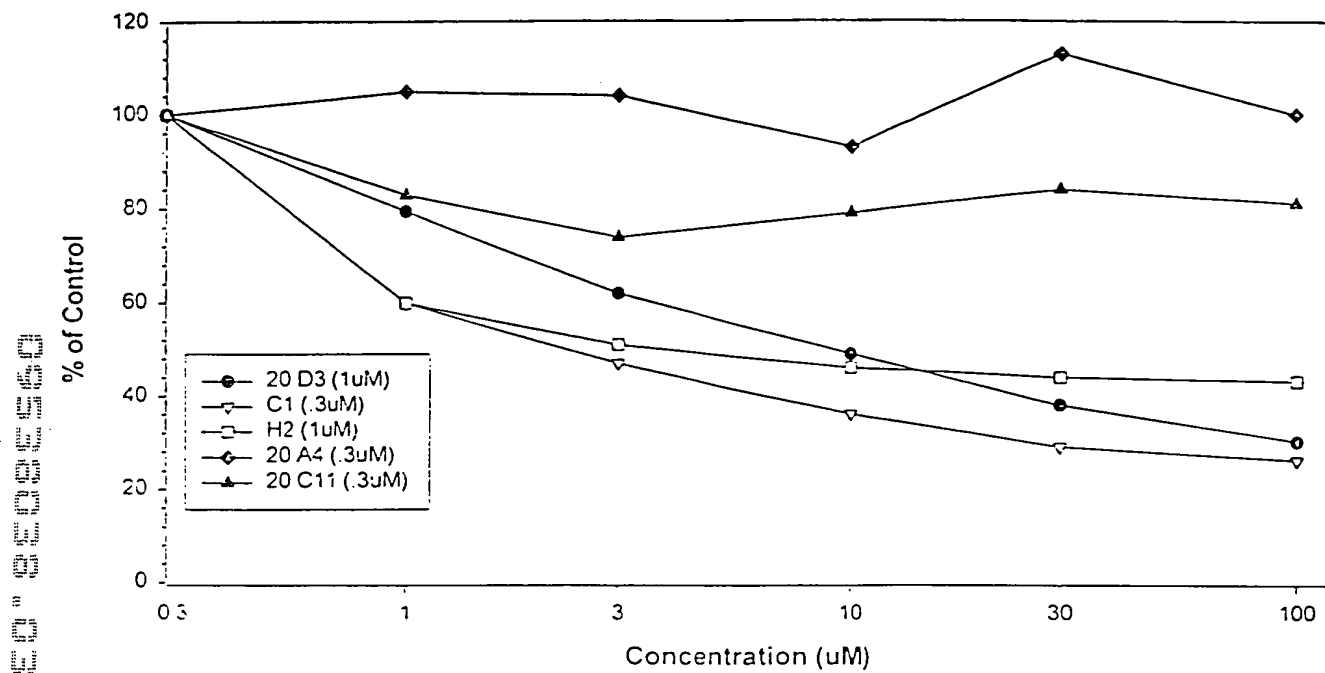


FIGURE 66

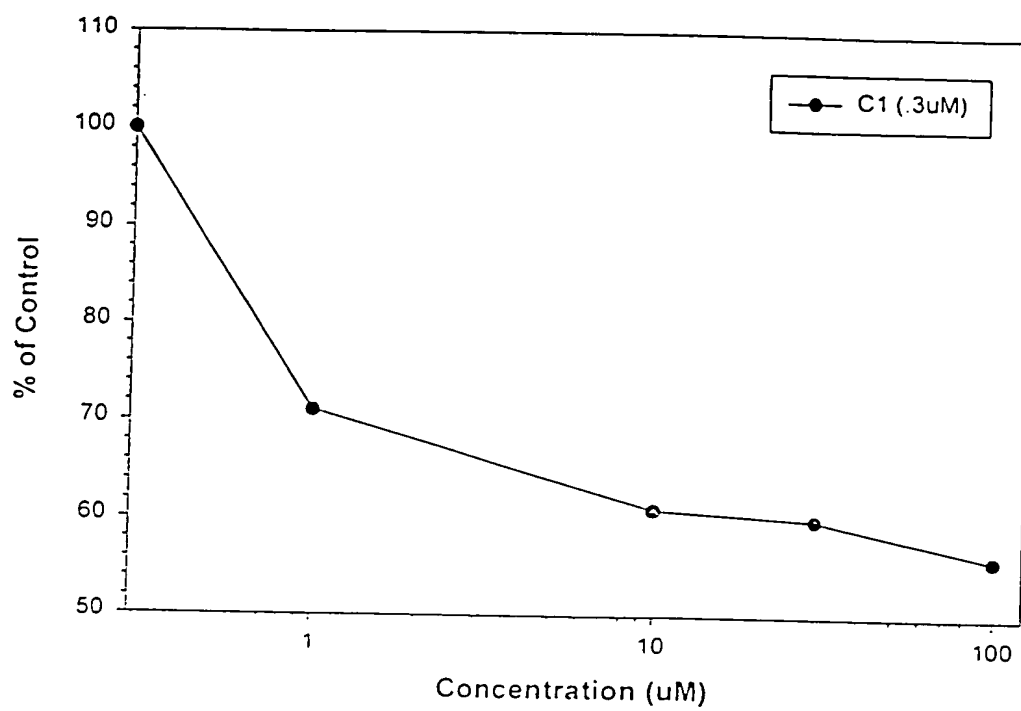


FIGURE 67

Concentration (uM)	C1 (%)	C1C (%)	H2C (%)	B5 (%)	GH (%)
0.1	100	100	100	100	100
0.5	98	92	98	98	102
1	83	126	105	98	112
5	71	90	68	112	118
10	52	74	45	95	103
30	38	58	44	94	80

FIGURE 68

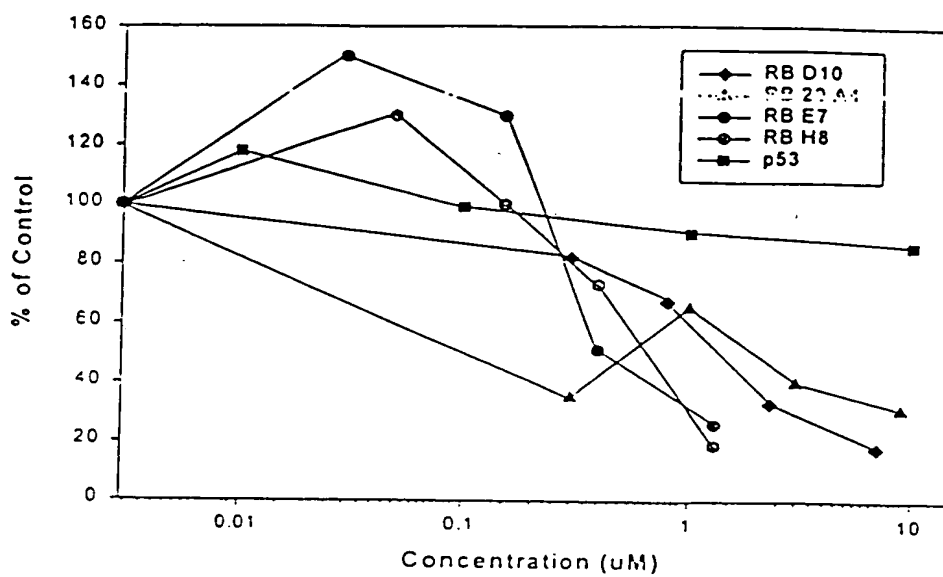


FIGURE 69



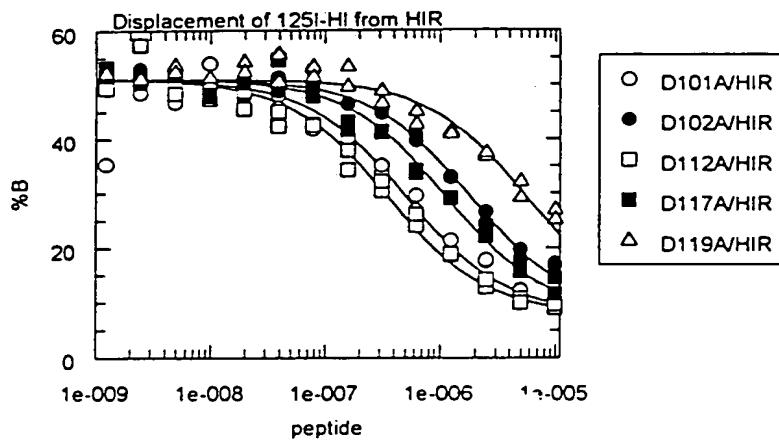


FIGURE 70A

D990114A

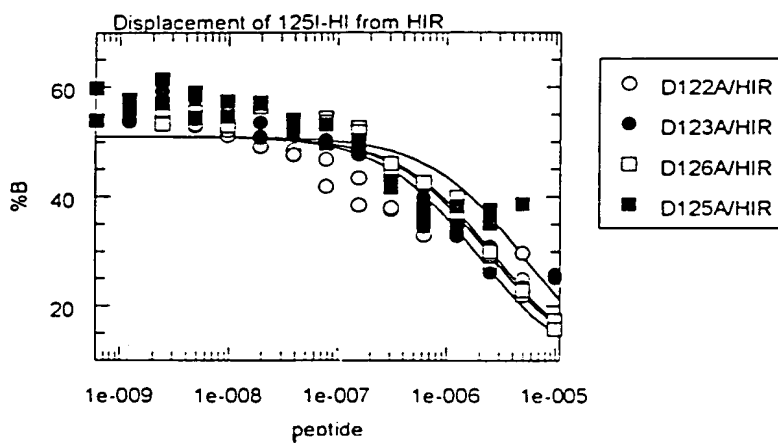


FIGURE 70B

D990118A

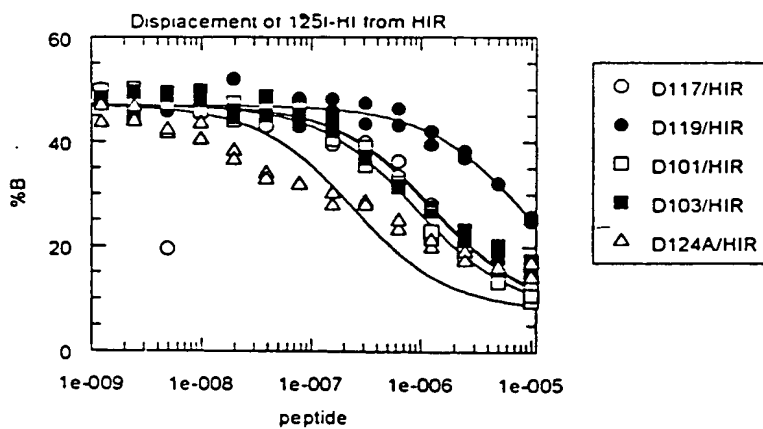


FIGURE 70C

D990126A

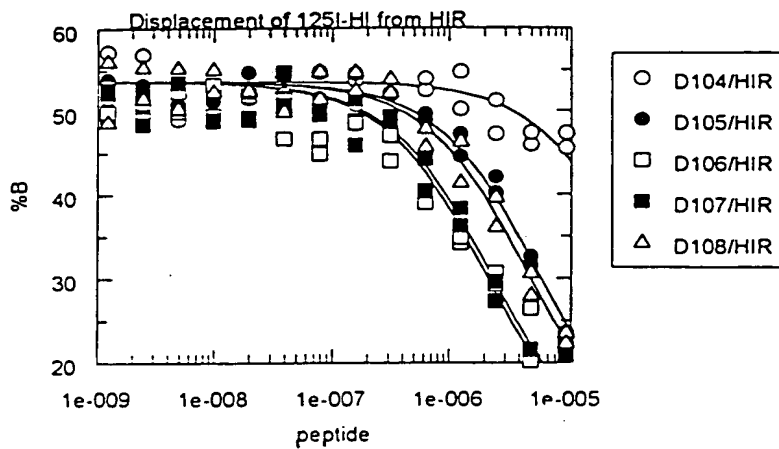


FIGURE 70D

D990129A

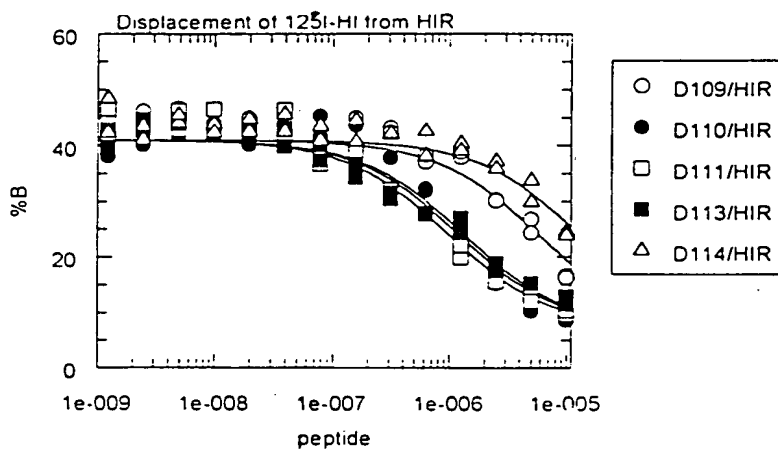


FIGURE 70E

D990202A

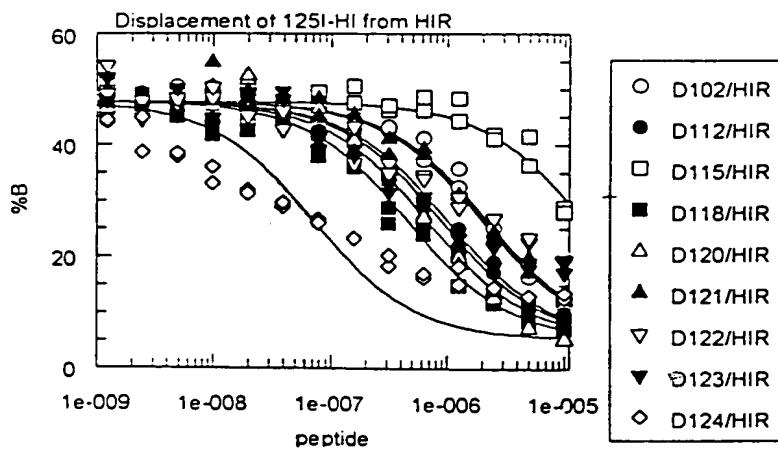


FIGURE 70F

D990205A

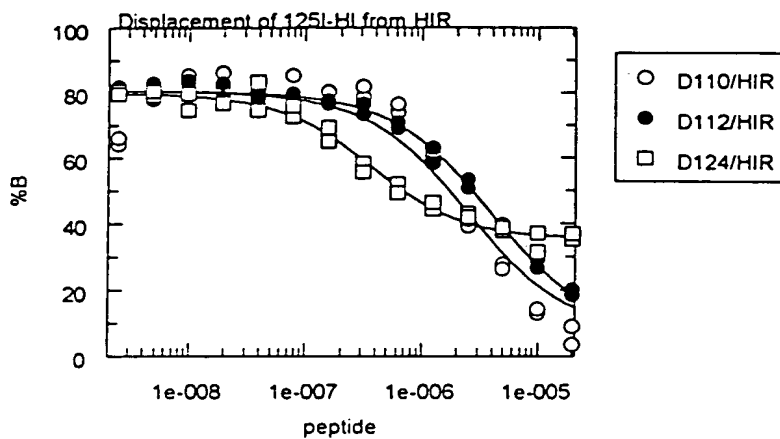


FIGURE 70G

D990217A

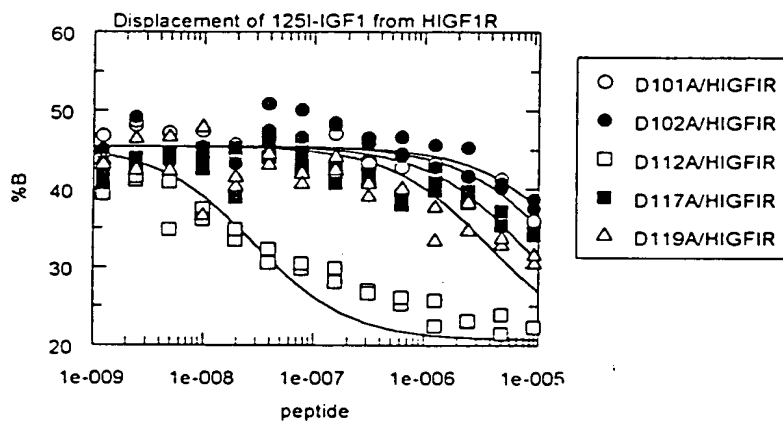


FIGURE 70H

D990114A

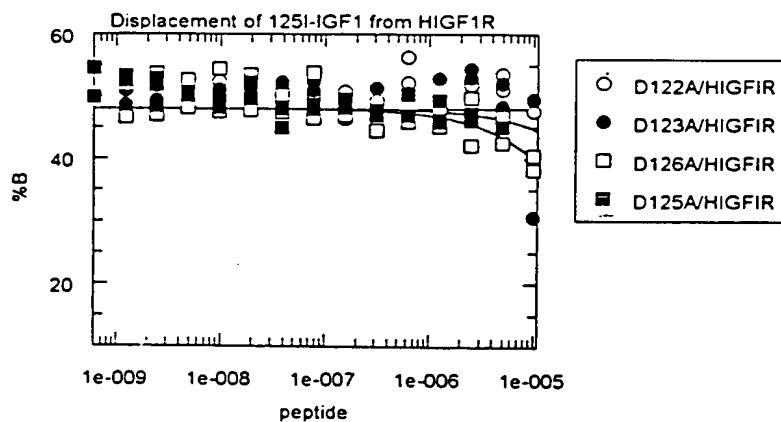
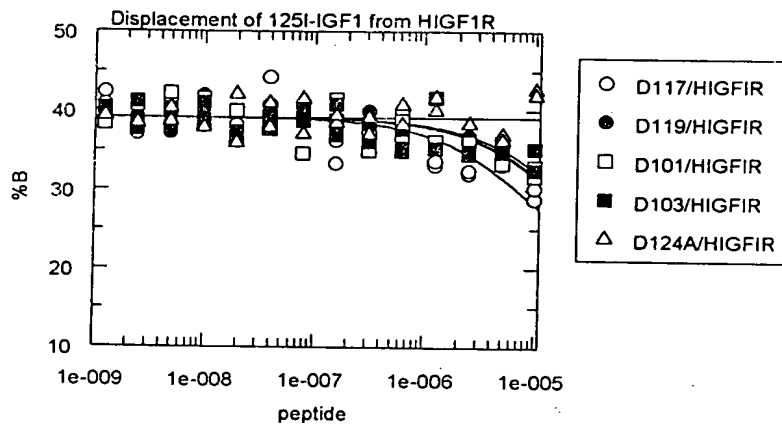


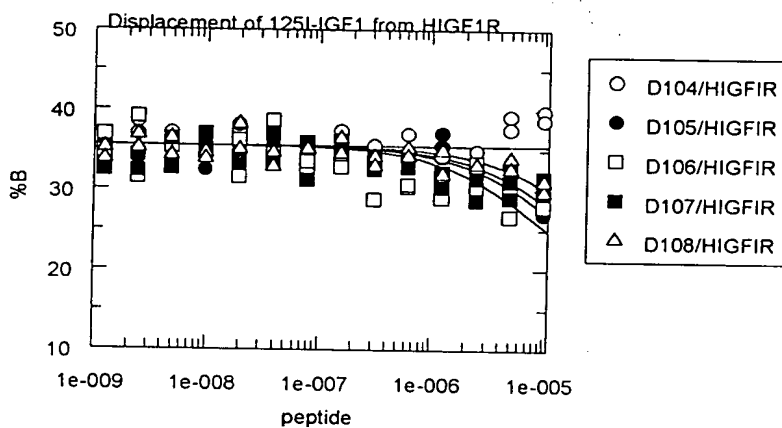
FIGURE 70I

D990118A



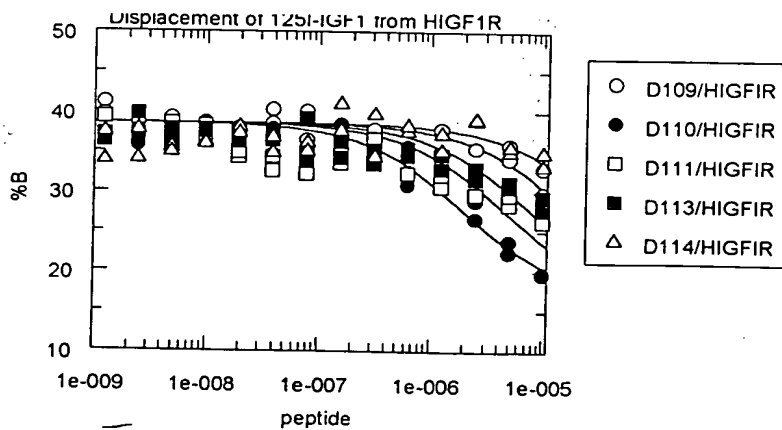
**FIGURE 70J**

D990126A



**FIGURE 70K**

D990129A



**FIGURE 70L**

D990202A

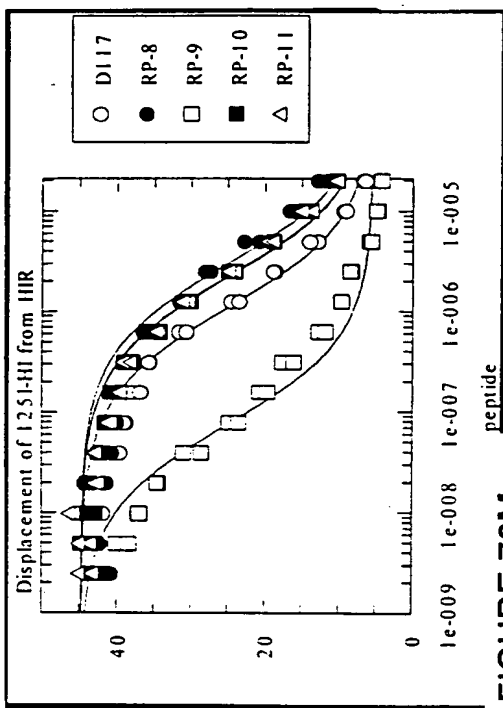


FIGURE 70M

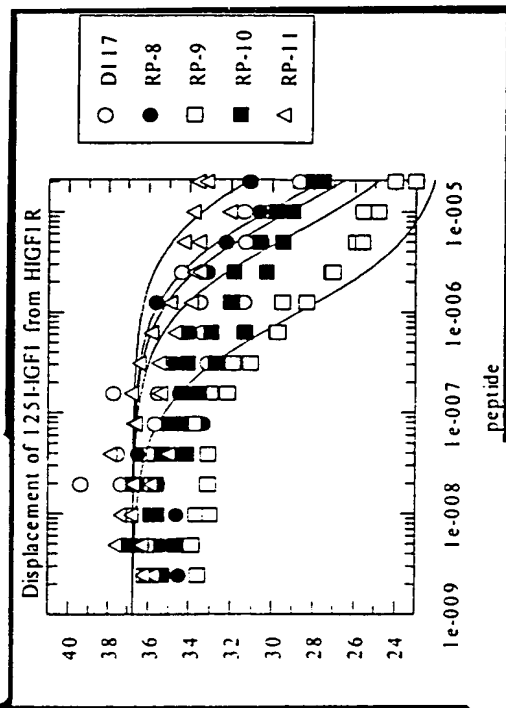


FIGURE 70N

FIGURE 71A

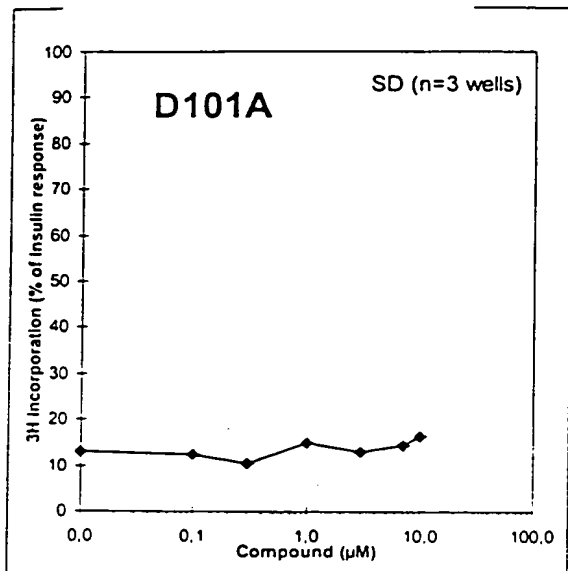


FIGURE 71B

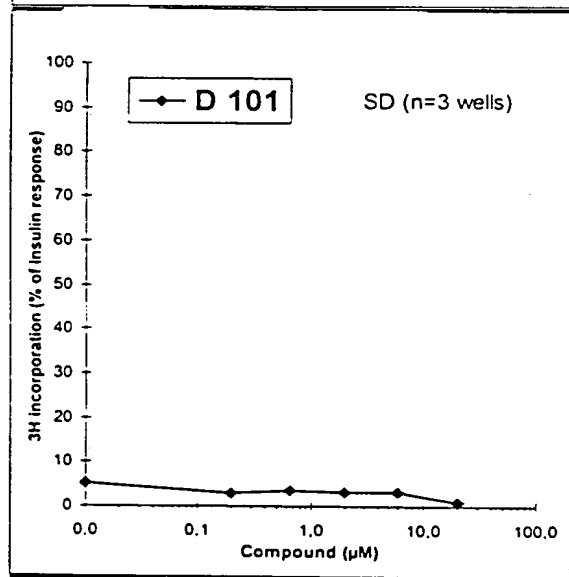
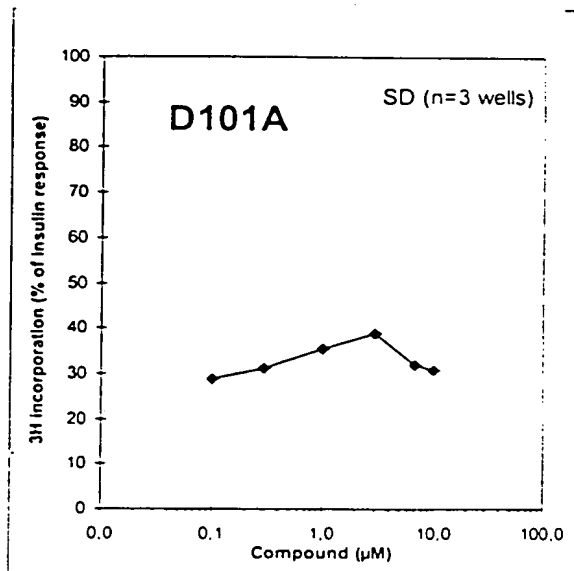


FIGURE 71C

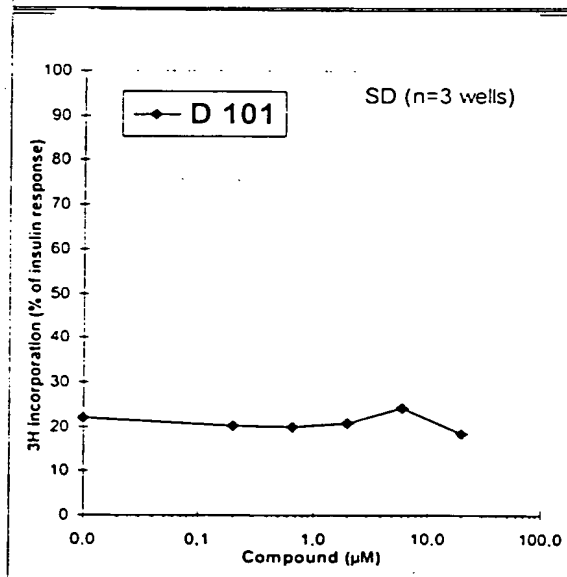


FIGURE 71D

FIGURE 71E

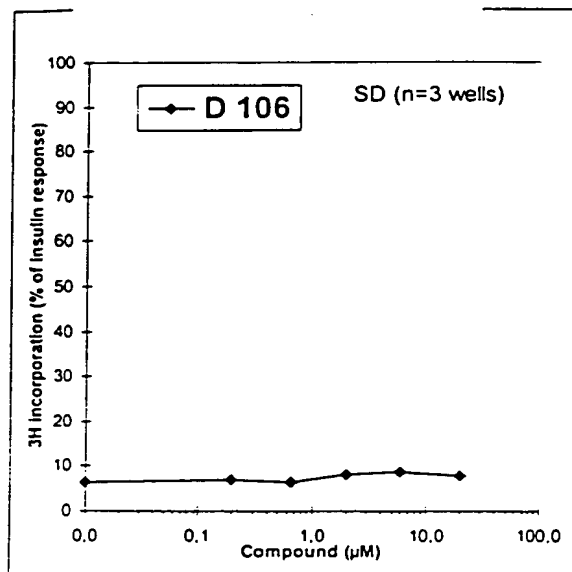


FIGURE 71F

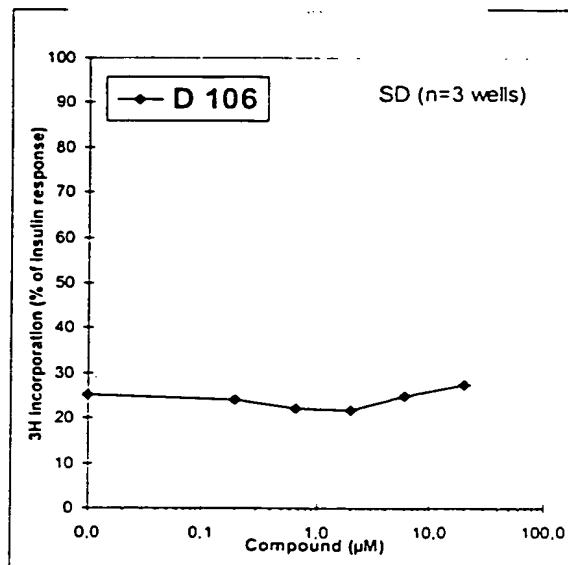


FIGURE 71G

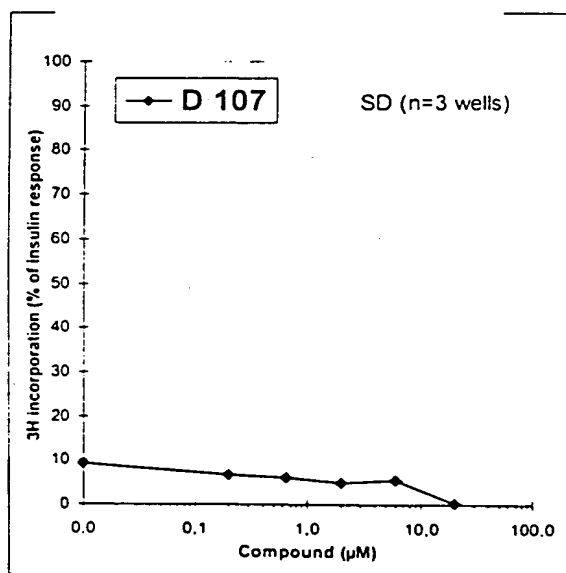


FIGURE 71H

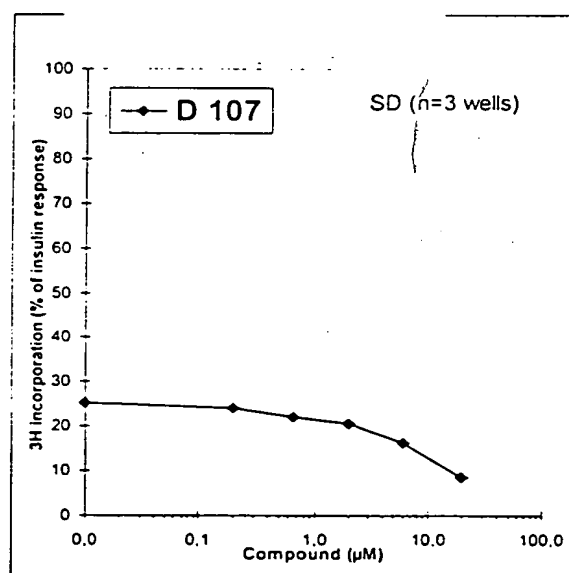


FIGURE 71I

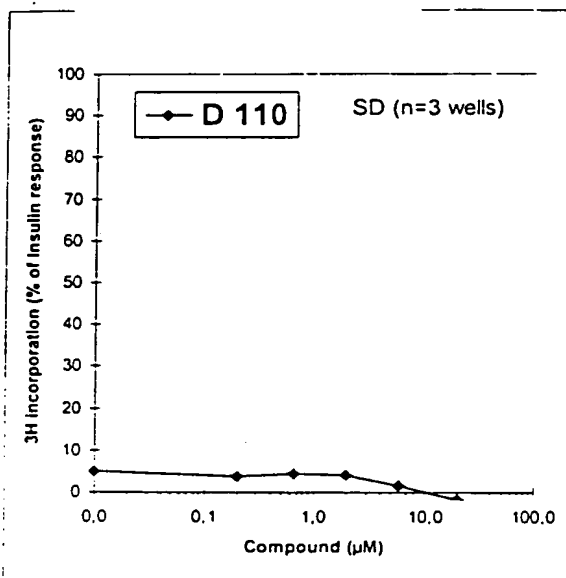


FIGURE 71J

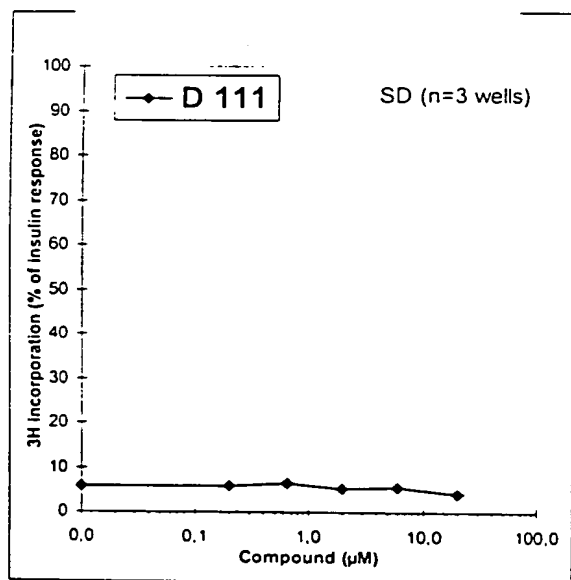
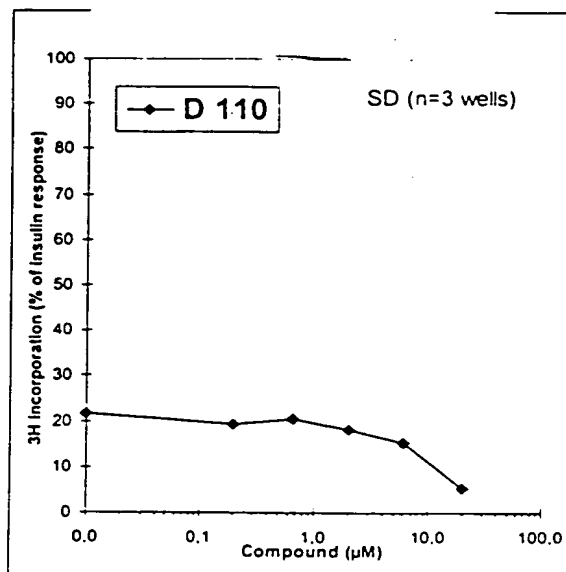


FIGURE 71K

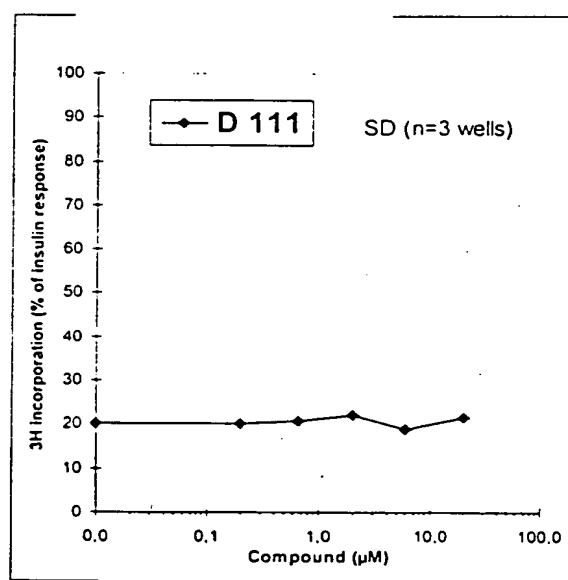


FIGURE 71L



FIGURE 71M

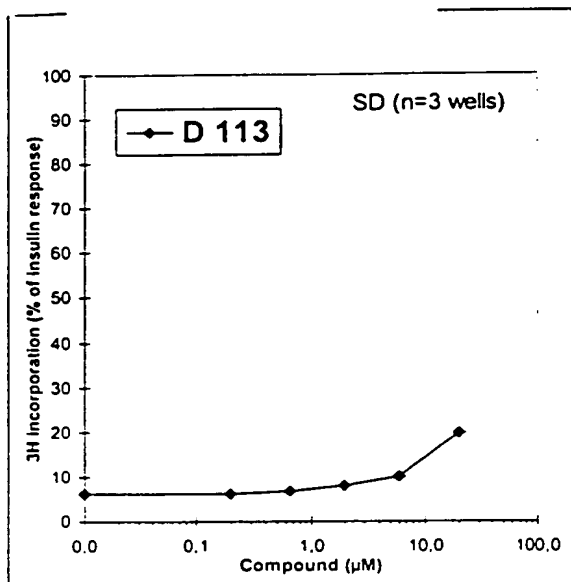


FIGURE 71N

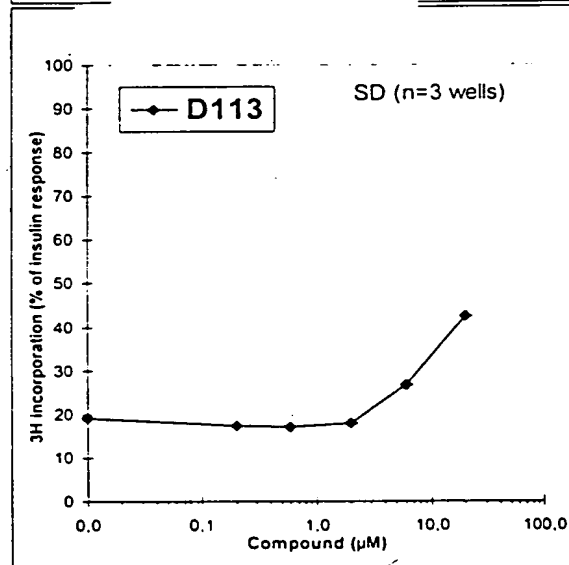
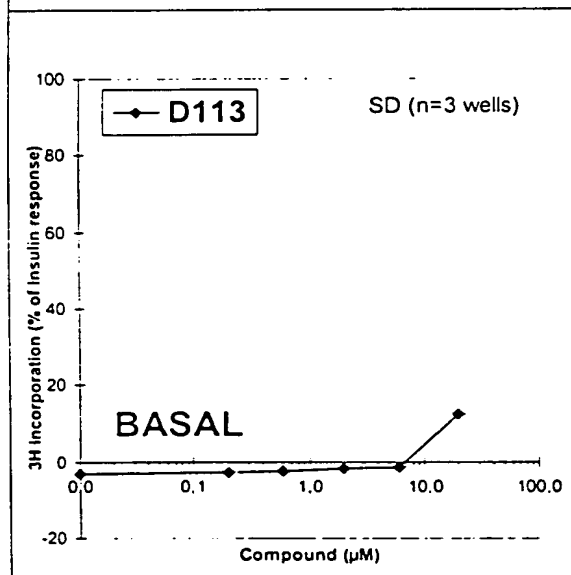
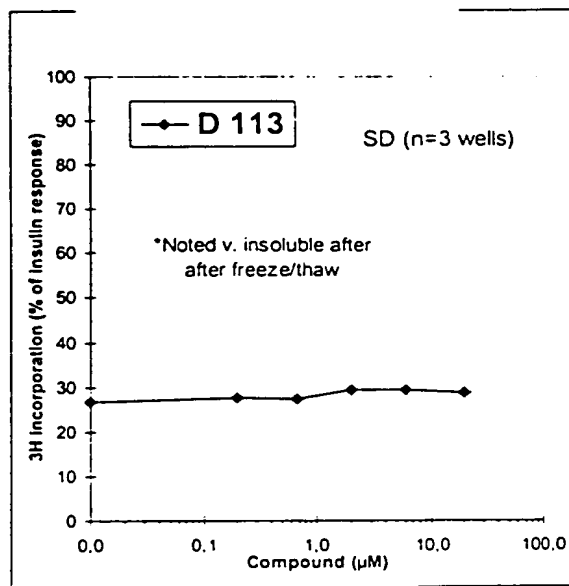


FIGURE 71O

FIGURE 71P

FIGURE 71Q

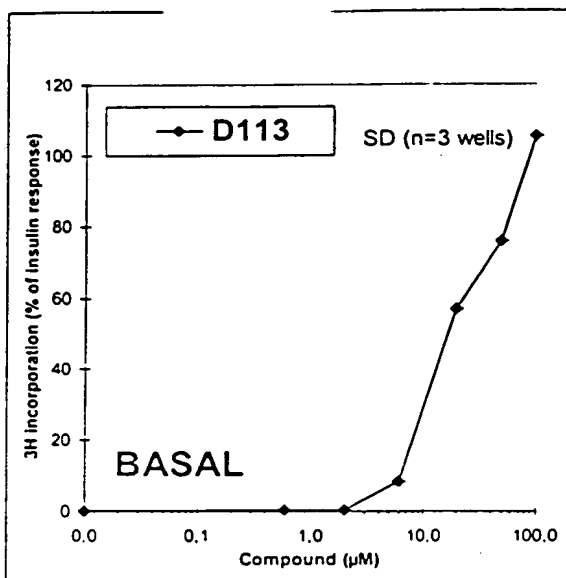


FIGURE 71R

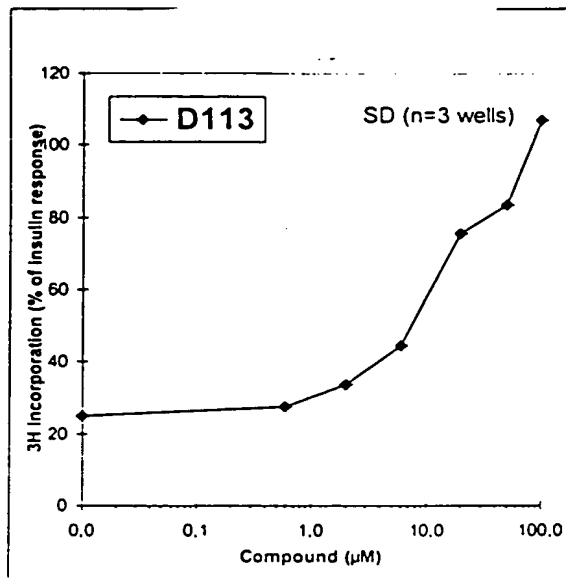


FIGURE 71S

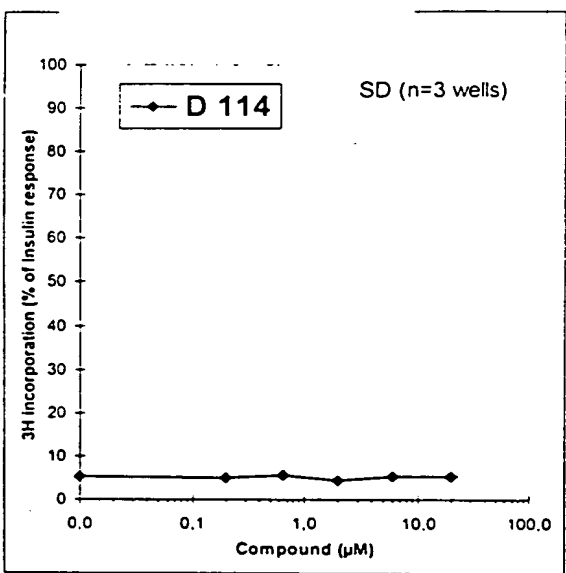


FIGURE 71T

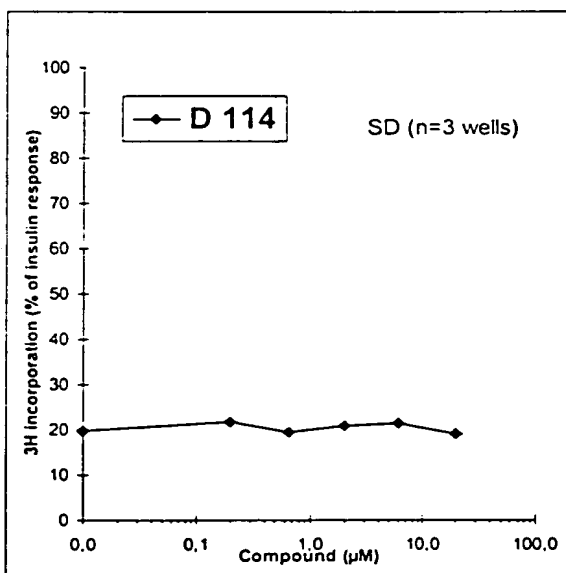


FIGURE 71U

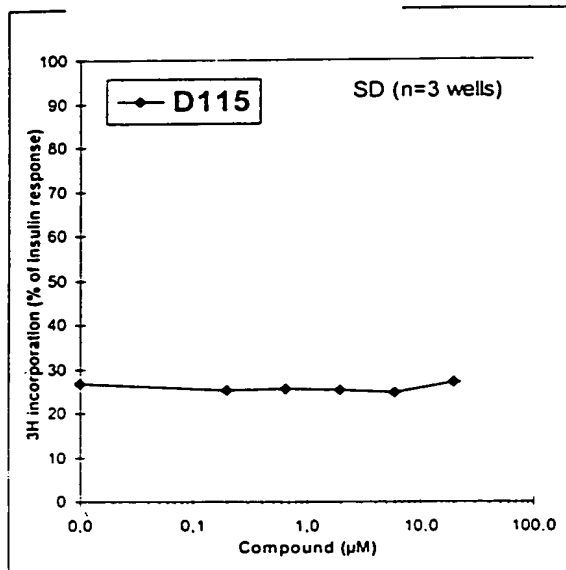


FIGURE 71V

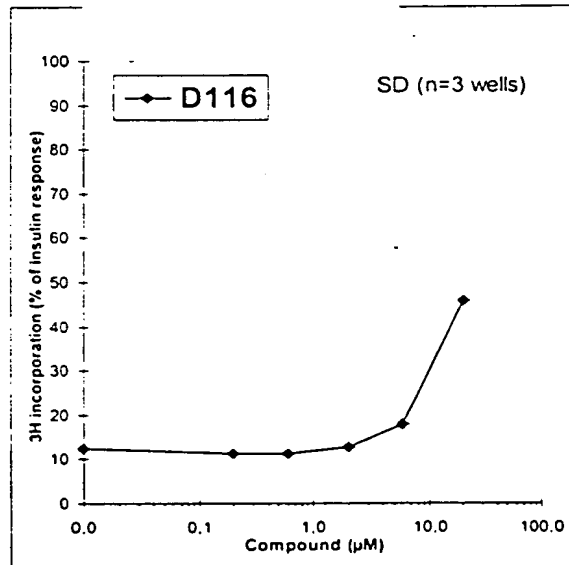
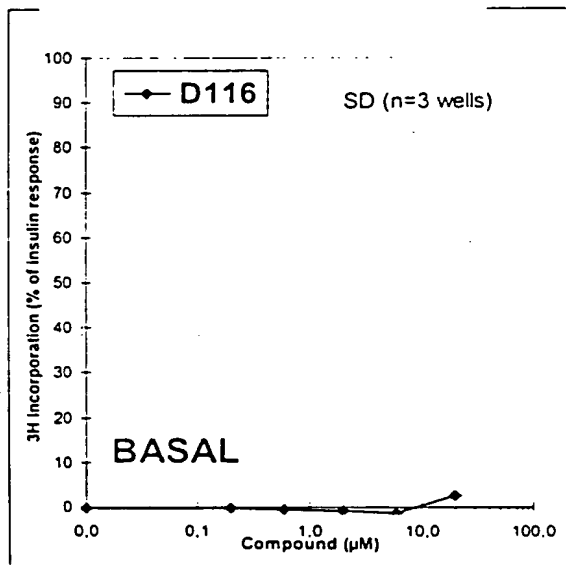
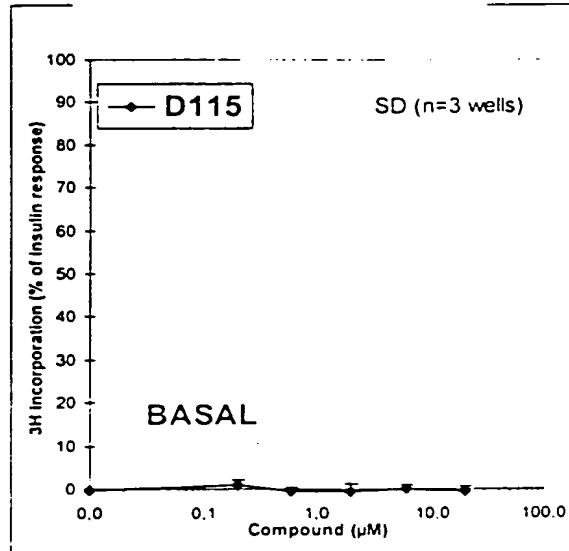


FIGURE 71W

FIGURE 71X

FIGURE 71Y

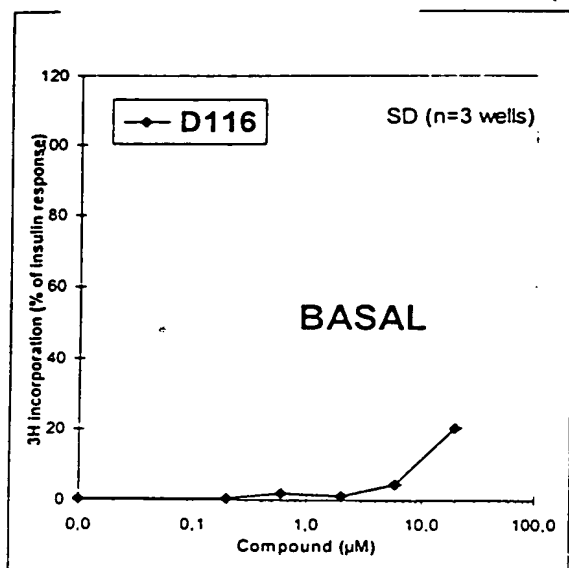


FIGURE 71Z

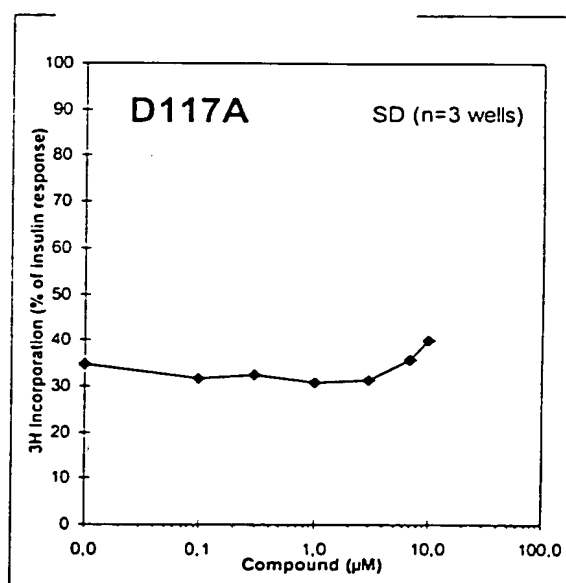
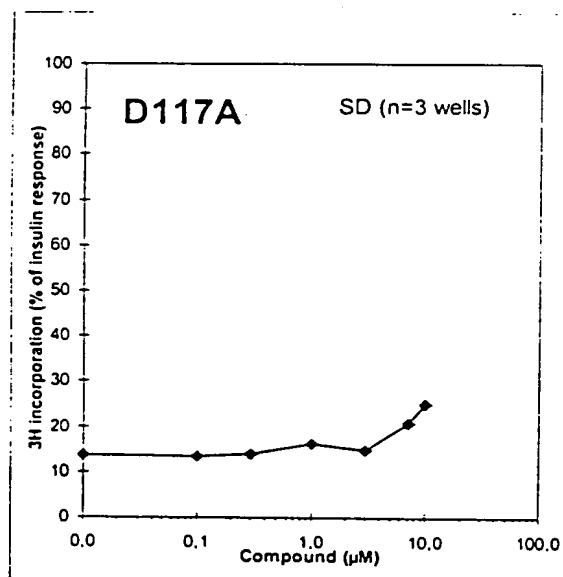
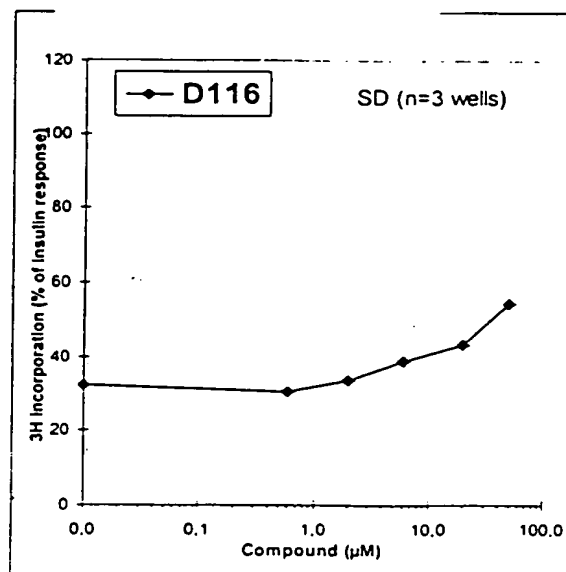


FIGURE 71A2

FIGURE 71B2

FIGURE 71C2

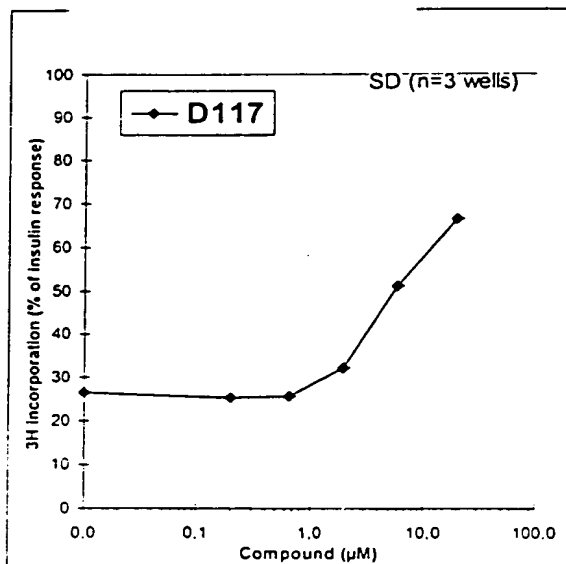


FIGURE 71D2

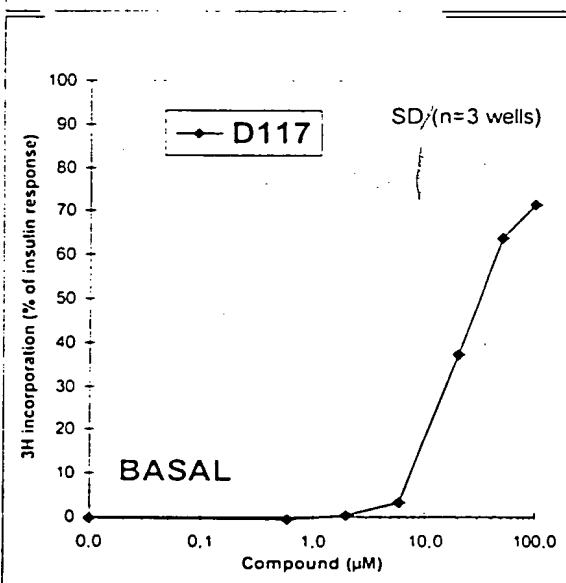
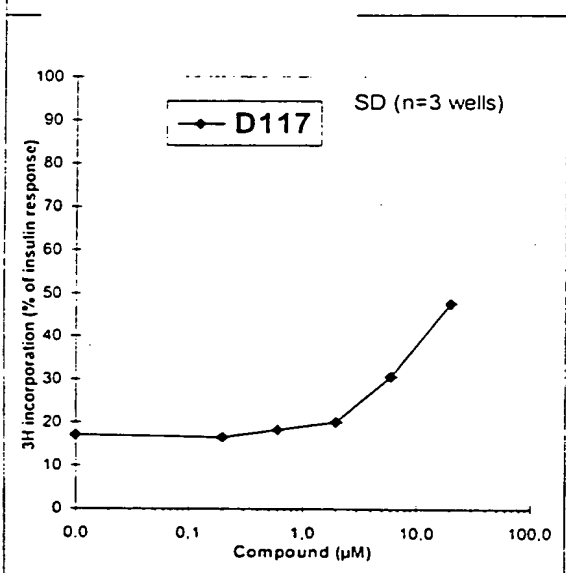
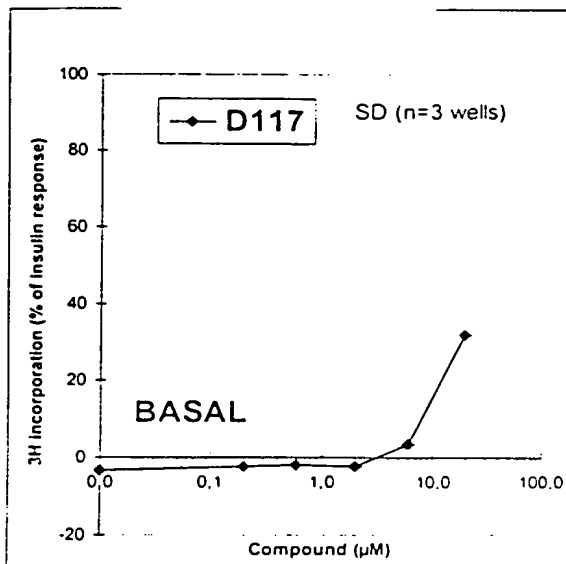


FIGURE 71E2

FIGURE 71F2

FIGURE 71G2

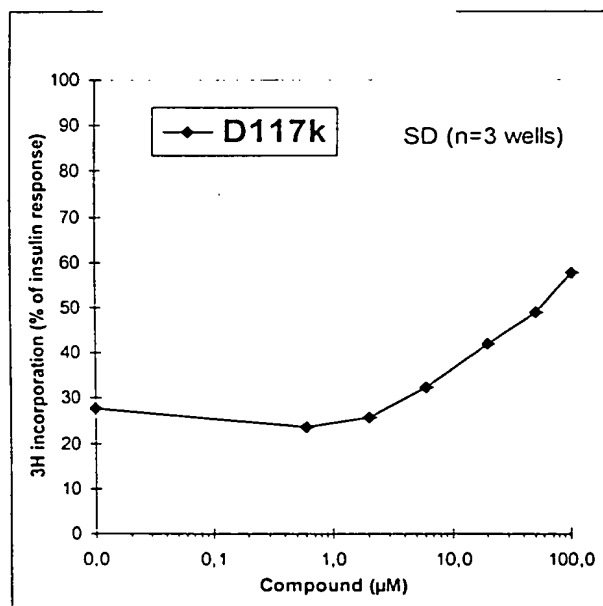
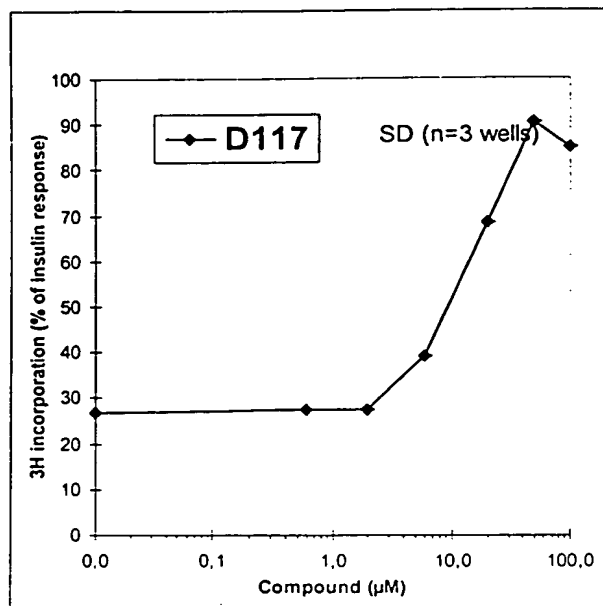


FIGURE 71H2

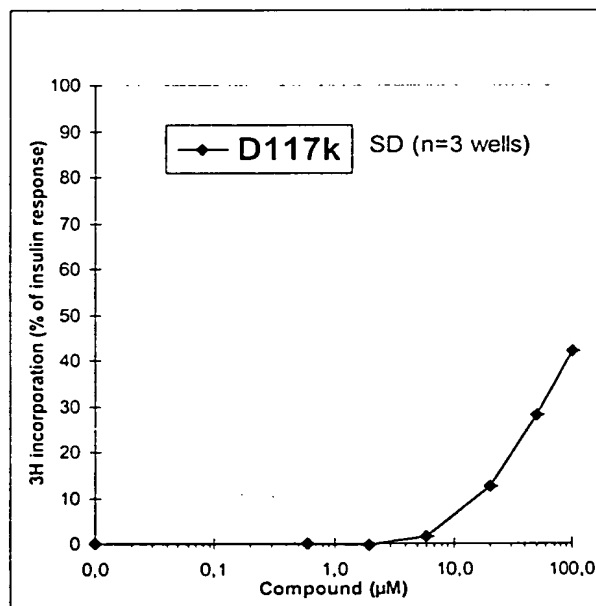


FIGURE 71I2

FIGURE 71J2

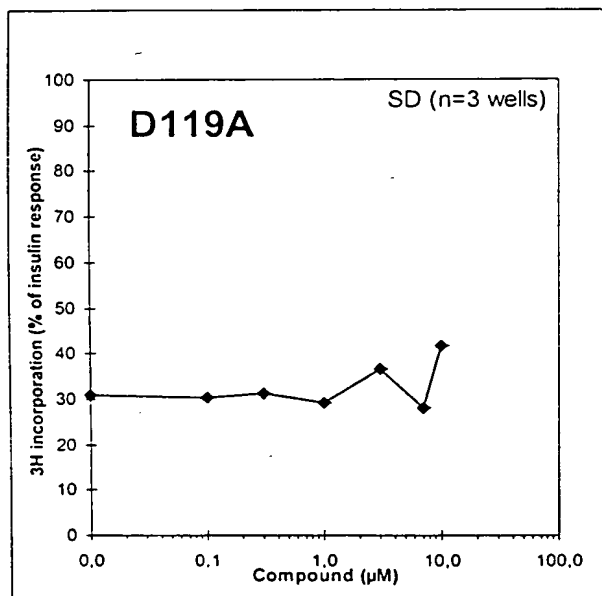
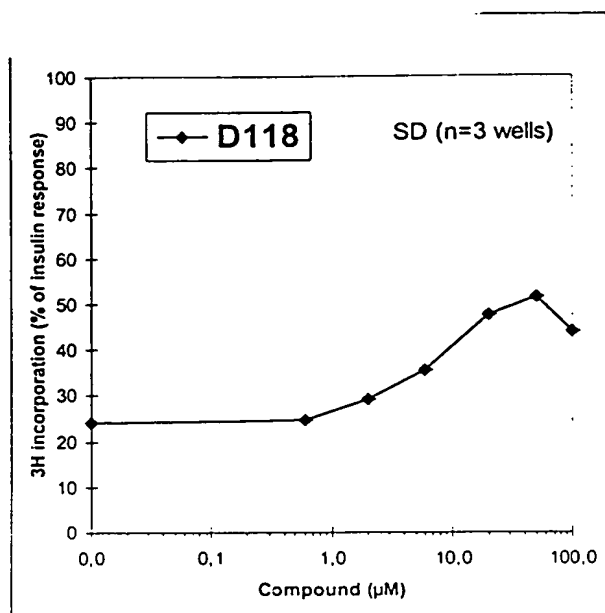


FIGURE 71K2

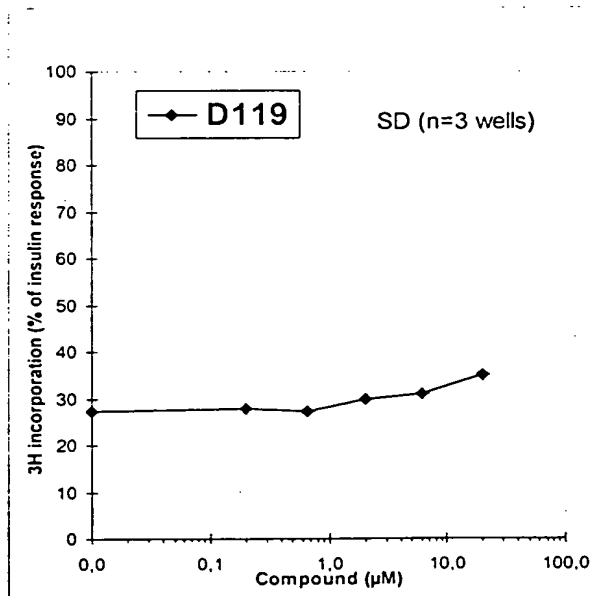


FIGURE 71L2

FIGURE 71M2

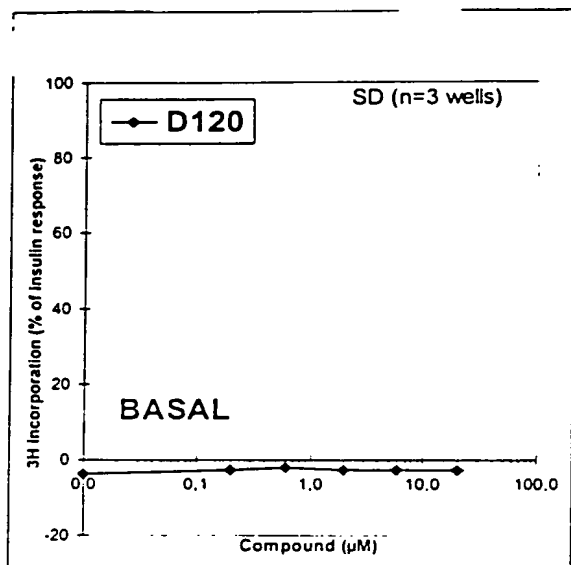


FIGURE 71N2

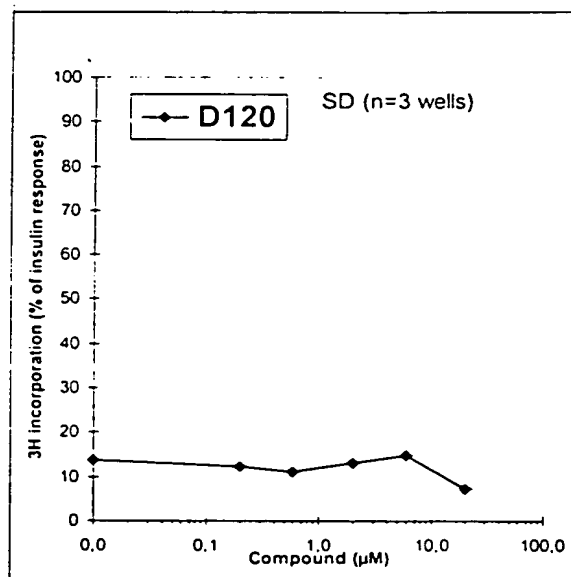
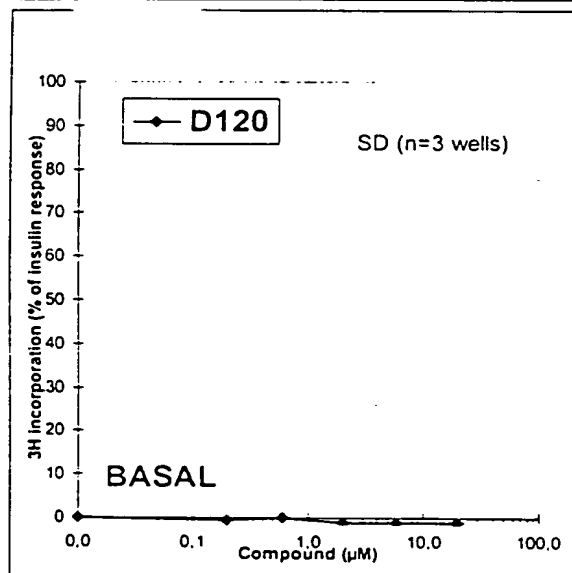
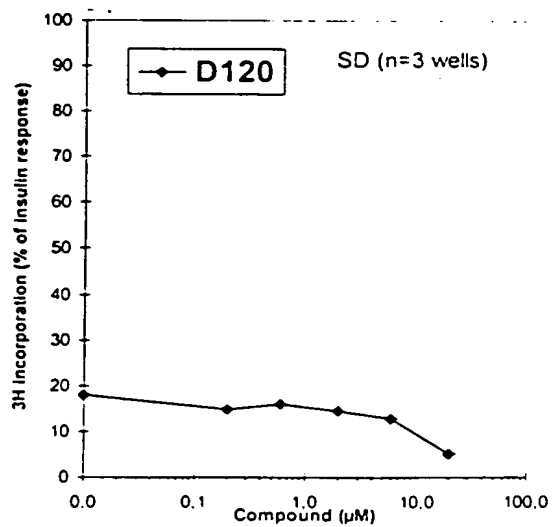


FIGURE 71O2

FIGURE 71P2



FIGURE 71Q2

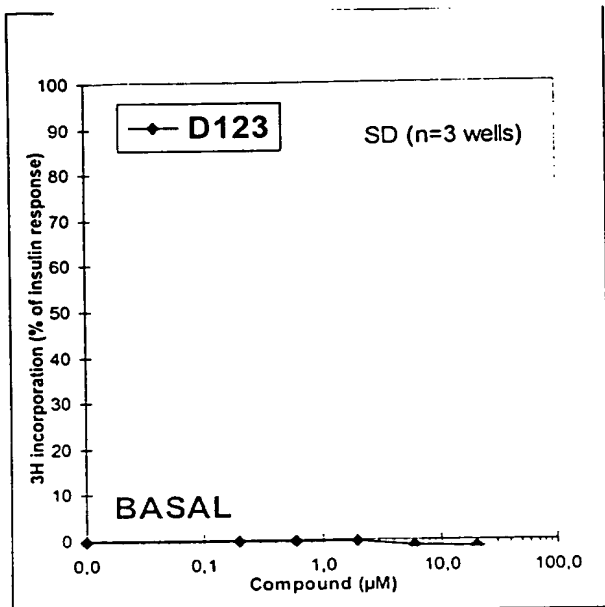


FIGURE 71R2

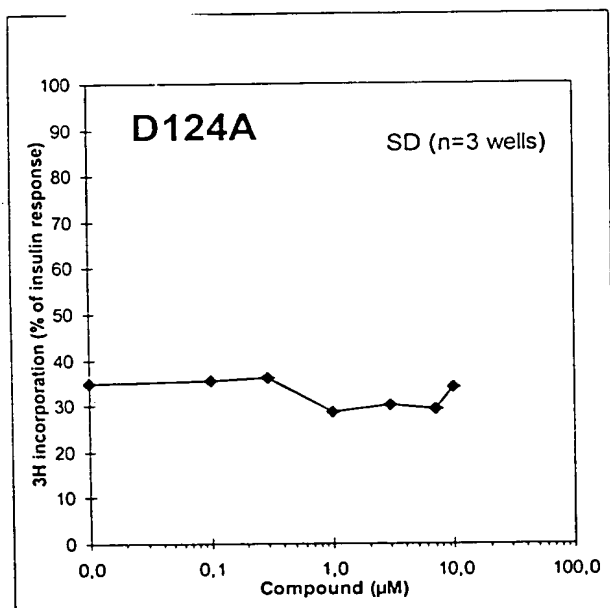
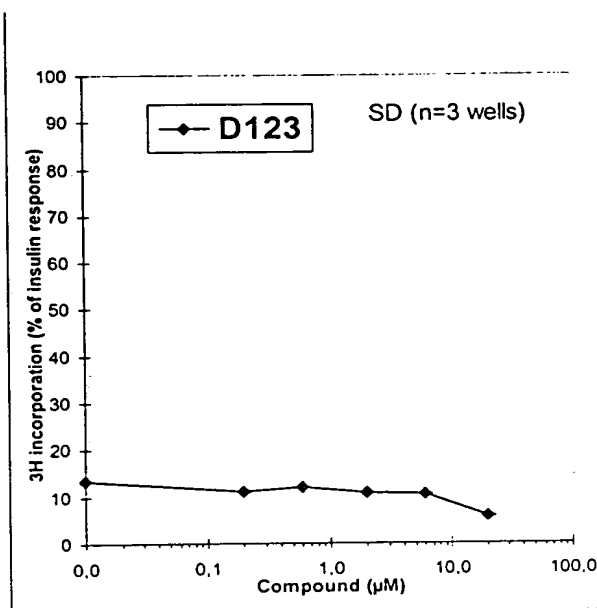


FIGURE 71S2

FIGURE 71T2

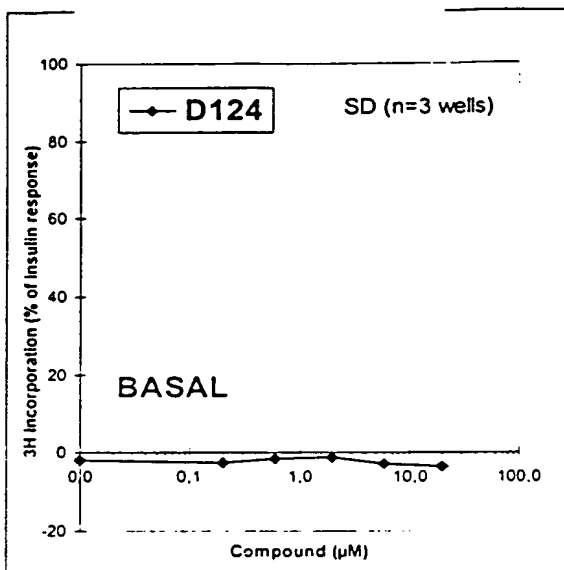


FIGURE 71U2

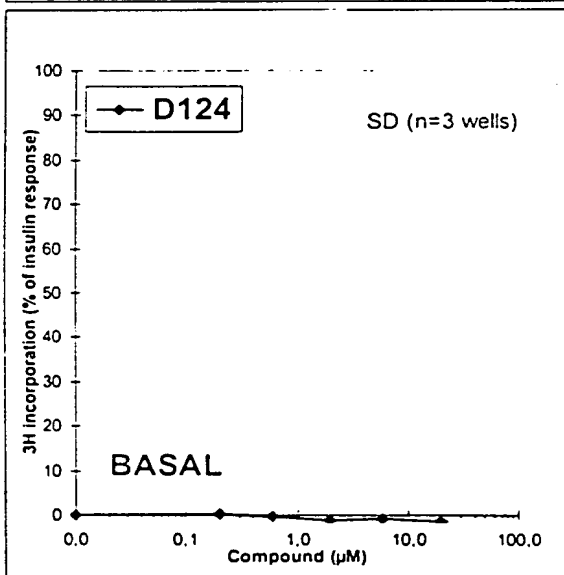
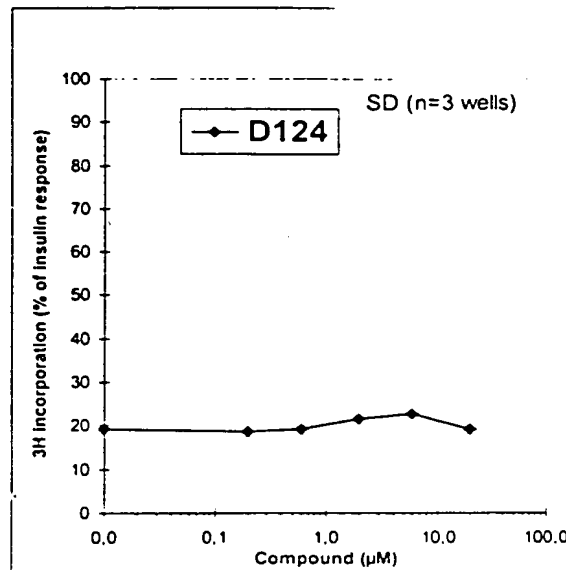


FIGURE 71V2

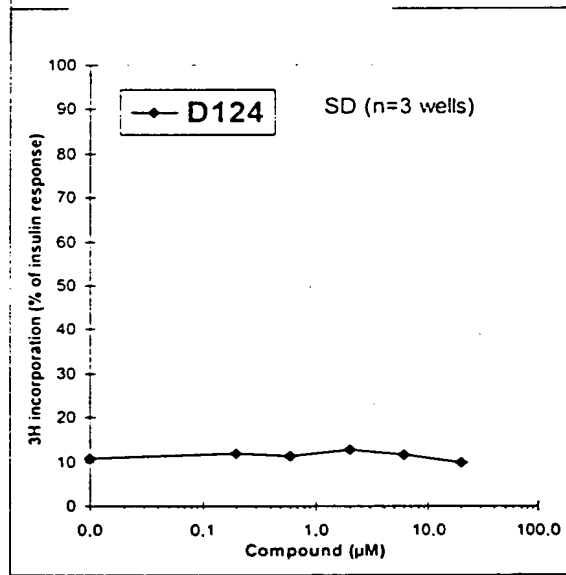


FIGURE 71W2

FIGURE 71X2

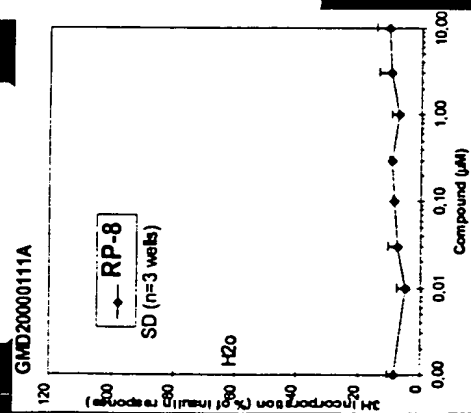


FIGURE 71Y2

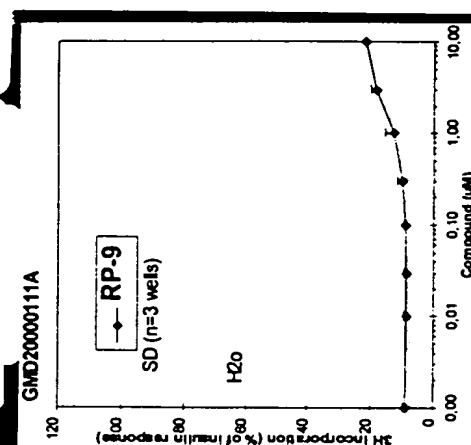


FIGURE 71Z2

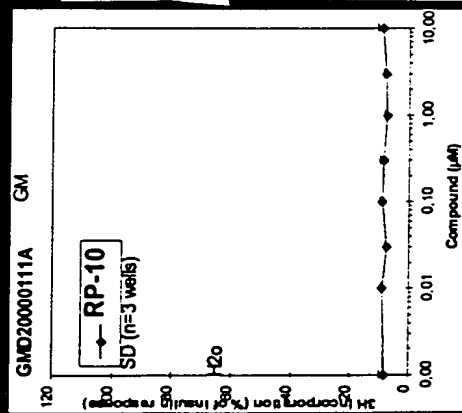
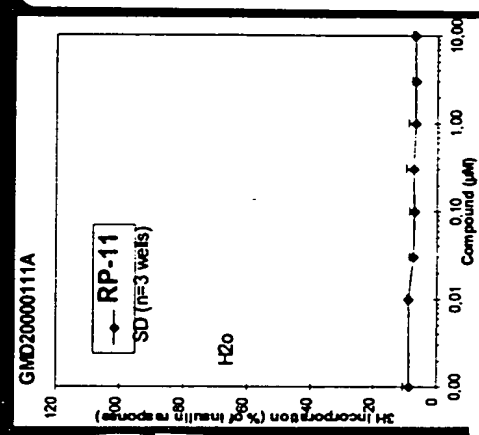
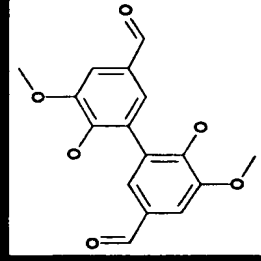


FIGURE 71A3



S291: Dimer of S204 with linker 9

S204 = Lig-GGGFHENFYDWFVRQVSKK



Linker 9 =

HIR binding =  $1.2 \times 10^{-6}$

FFC:

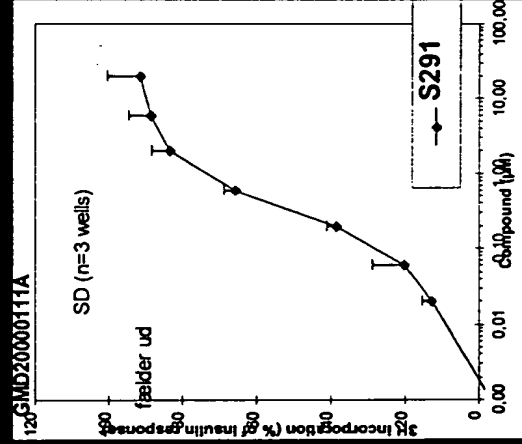
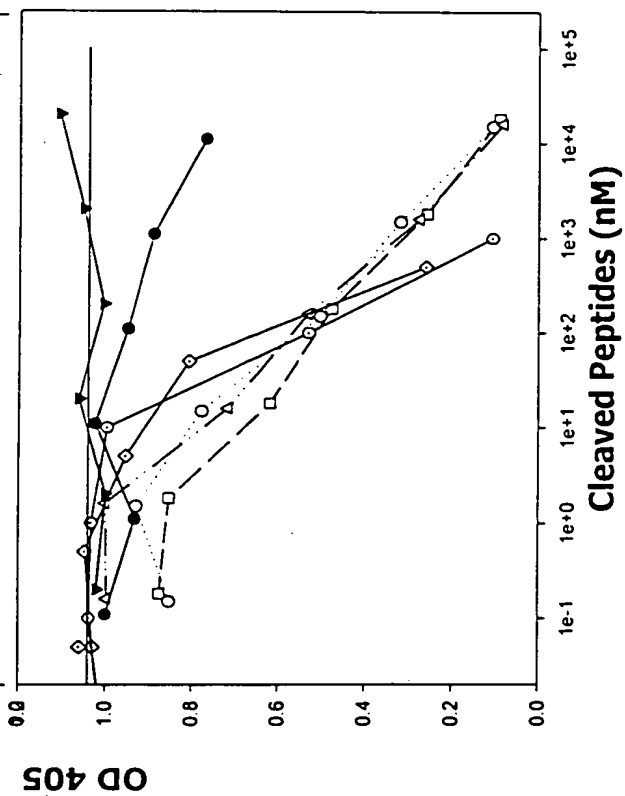


FIGURE 71B3

Figure 1 is a line graph showing the effect of various peptides on the release of  $^{125}$ I-labeled lacZ from m8p control cells. The y-axis represents OD 405 (0.2 to 1.2) and the x-axis represents time in minutes (0 to 120). A vertical line at 30 minutes indicates the addition of 100% value of  $^{125}$ I-labeled lacZ. The legend includes: Cleaved mono / di-peptide (filled triangles), LFF8 (filled squares), F8 peptide (open diamonds), LFH2C (open circles), LFH2C(9)/F8 (open squares), LFFH2C(6)/F8 (open triangles), LFH2C(12)/F8 (open circles with a dot), and LFH2C (open circles). The graph shows that the release of  $^{125}$ I-labeled lacZ increases over time for all conditions. The LFH2C(9)/F8 condition shows the highest release, reaching an OD 405 of approximately 1.1 at 120 minutes. The LFH2C(12)/F8 condition shows the lowest release, reaching an OD 405 of approximately 0.2 at 120 minutes.



**FIGURE 72B**

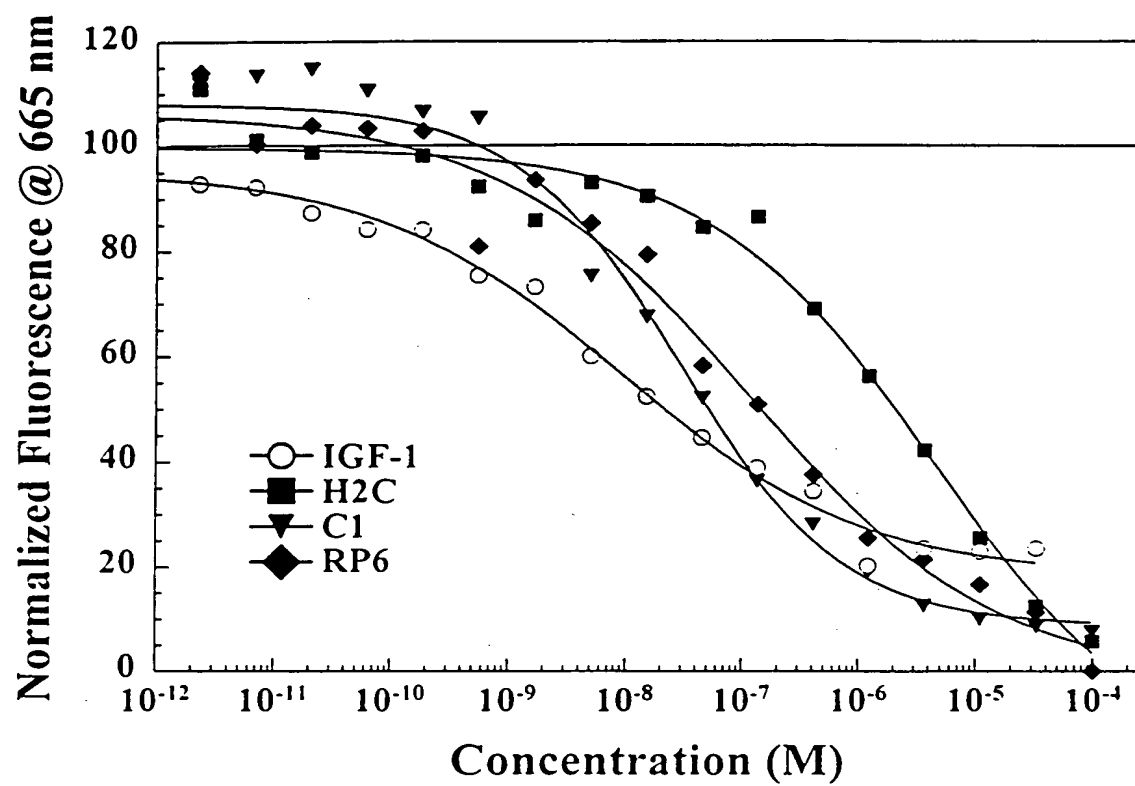


FIGURE 73



FIGURE 74